

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 28, 2005, 00:40:20 ; Search time 13971 Seconds
(without alignments)
7931.936 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVRCVRRTPPLRGSAR.....KKDTLSLGLSSDPTDMDPZ 2287

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_un.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12024	100.0	7540	6	AX068898 Sequence
2	11980	99.6	6942	10	AF290212 Rattus no
3	11980	99.6	7542	10	AF027984 Rattus no
4	11829	98.3	7285	6	BD224079 T-type ca

	5	11829	98.3	7286	10	AF125161
	6	11673	97.0	7129	6	BD224078 T-type ca
	7	11592.5	96.4	7625	10	MMU012569 Mus muscu
	8	11489	95.5	7527	10	BC057399 Mus muscu
	9	11088	92.2	7274	9	AF126966 Homo sapi
	10	11088	92.2	7349	9	AF190860 Homo sapi
	11	11066.5	92.0	7741	6	AR201015 Sequence
	12	11037.5	91.8	7253	9	AF126965 Homo sapi
	13	10948.5	91.0	6822	6	AR201014 Sequence
	14	10948.5	91.0	6822	9	AF227744 Homo sapi
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	16	10923.5	90.8	6786	9	AF227747 Homo sapi
	17	10914.5	90.7	6966	9	AF227745 Homo sapi
	18	10902	90.6	6855	9	AF227749 Homo sapi
	19	10898	90.6	6801	9	AF227751 Homo sapi
	20	10891	90.5	6921	9	AF227748 Homo sapi
	21	10868	90.4	6999	9	AF227750 Homo sapi
	22	10845.5	90.2	7648	9	AF134986 Homo sapi
	23	10631.5	88.4	7030	9	AF134985 Homo sapi
	24	10626.5	88.3	7030	6	CQ724231 Sequence
	25	8137	67.7	5475	9	AB032949 Homo sapi
	26	7256.5	60.3	4903	9	AB012043 Homo sapi
	27	6809.5	56.6	4944	10	AK129294 Mus muscu
	28	6248	51.9	8447	6	AX068900 Sequence
	29	6242	51.9	7898	6	BD087035 Calcium c
	30	6242	51.9	7898	9	AF073931 Homo sapi
	31	6241	51.9	7898	6	BD087032 Calcium c
	32	6240	51.9	7762	9	AF051946 Homo sapi
	33	6235.5	51.8	7868	10	AF290213 Rattus no
	34	6233	51.8	7044	9	HS4420779 Homo sapi
	35	6103	50.7	3993	9	AF124351 Homo sapi
	36	5738.5	47.7	6941	6	BD087036 Calcium c
	37	5596.5	46.5	6924	6	CQ730788 Sequence
	38	5441	45.2	6911	10	AF086827 Rattus no
	39	5432.5	45.2	6990	9	AF142567 Homo sapi
	40	5420	45.1	6816	6	AR175747 Sequence
	41	5420	45.1	6816	6	AR352550 Sequence
	42	5420	45.1	6855	6	AR175748 Sequence
	43	5420	45.1	6855	6	AR352551 Sequence
	44	5420	45.1	9896	9	AF393329 Homo sapi
	45	5407	45.0	6503	6	AR175755 Sequence

ALIGNMENTS

RESULT 1	AX068898	Sequence 23 from Patent WO0102561.	7540 bp	DNA	linear	PAT 25-JAN-2001
LOCUS	AX068898	Sequence 23 from Patent WO0102561.	7540 bp	DNA	linear	PAT 25-JAN-2001
DEFINITION	AX068898	Sequence 23 from Patent WO0102561.	7540 bp	DNA	linear	PAT 25-JAN-2001
ACCESSION	AX068898	Sequence 23 from Patent WO0102561.	7540 bp	DNA	linear	PAT 25-JAN-2001
VERSION	AX068898.1	GI:12578748	7540 bp	DNA	linear	PAT 25-JAN-2001
KEYWORDS	AX068898.1	GI:12578748	7540 bp	DNA	linear	PAT 25-JAN-2001
SOURCE	Rattus sp.					
ORGANISM	Rattus sp.					
REFERENCE	1	Snutch, T.P. and Baillie, D.L.				
AUTHORS	1	Snutch, T.P. and Baillie, D.L.				
TITLE	1	Mammalian calcium channels and related probes, cell lines and methods				
JOURNAL	1	Patent: WO 0102561-A 23 11-JAN-2001;				
FEATURES	1	Neuromed Technologies, Inc. (CA)				
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ORIGIN

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Score:

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.97%	Indels:	0
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DB	385	ATGCTCCCCACCGGTGCTCCCGGTTGGTGGAGACACCTCTCTGAGGGGCTCCGCTCGC	444
QY	21	ProSerSerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGlu	40
DB	445	CCCTCTCCGAGCCCCCGGGGCCCCGGCTGGCCAGAGATGACGAGGAGGAGATGGAG	504
QY	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly	60
DB	505	CGGGGCCCGAGGATCGGGACAGCCCGCTAGCTTCAGCGAGCTCAACGACCTGTCCGGGG	564
QY	61	ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla	80
DB	565	CGGGGGCGGCGAGGGCCGGTCCAGCGAAAGGACCCGGGCGAGCGGACTCCGAGGCG	624
QY	81	GluGlyLeuProTyrProAlaAlaProValAlaProValAlaPhePheTyrLeuSerGlnAspSer	100
DB	625	GAGGGGCTGCCGFPACCCGGCGCTAGCCCCGGTGGTTTTCTTCTACTTGGACCGAGACGC	684
QY	101	ArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValSerMet	120
DB	685	CGCCCGGGAGCTGGTGTCTCCGACCGGTCTGTAAACCCGTTGTCGAGCGAGTCAAGTATG	744
QY	121	LeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	140
DB	745	CTGGTCAATTTCTCAACTGTGTGACTCTGGGTATGTTTTCAGGCGGTGTGAGGACATGGC	804
QY	141	CysAspSerGlnArgCysArgGlyLeuGlnAlaPheAspPheIlePheAlaPhePhe	160
DB	805	TGTGACTCCCGAGCGCTGCCGATCTTCGAGCGCTTCGATGACTTCACTTTCCTTCTTT	864
QY	161	AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu	180
DB	865	GCTGTGAAATGGTGTGTAAGATGGTGGCTTCGGCATCTTTTGGGAGAAATGTTACCTG	924
QY	181	GlyAspThrThrPheAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer	200
DB	925	GGAGACACTTGGAAACCGCTTGACTTTTTCATTTGTCATTCGACGGATGCTGGAGTATCG	984
QY	201	LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu	220
DB	985	CTGGACCTGCAGAACGTCAGCTTCTCCGCACTCAGGACAGCTCCGCTGTGCTGCGACCGCTC	1044
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuLeuLeuLeuLeu	240
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QY	241	ProMetLeuGlnAsnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	260
DB	1105	CCATGCTGGGCAACGCTTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG	1164
QY	261	GlyValGlnLeuThrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
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QY	281	LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro	300
DB	1225	CTCCCGCTGAGCGGAGCTGAGCGCTTATTCAGACAGAGATGAGGACGAGAGCCCC	1284
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
DB	1285	TTCATCTGCTCTAGCGCTCGGAGATGGCATGAGATCCCTGCGAGAGTGTGCCCACTG	1344
QY	321	ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrThrAsnSerSer	340
DB	1345	CGTGGGAGAGCGGTGGTGGCCACCCTGCGAGTCTGGACTATGAGACCTATAACAGTTCC	1404
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DB	1405	AGCAACACCACTGTGTCAACTGGAACCACTATATACCAACTGCTCTGGGGGAGAC	1464
QY	361	AsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaThrIleAlaIlePhe	380
DB	1465	AACCCCTTCAAGAGCGCATCACTTTCAGCAACATTTGGCTATGCTGGATCGCCATCTTC	1524
QY	381	GlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSer	400
DB	1525	CAGTTCATCACACTGGAGGGCTGGTCCGACATCATGTACTTCTGTAATGGAGCTCACTCC	1584
QY	401	PheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsn	420
DB	1585	TTCTACAACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1644
QY	421	LeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu	440
DB	1645	CTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	1704
QY	441	MetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlu	460
DB	1705	ATGGGGAGCAGCGGTGACGATTTCTGTCCAATGCTAGCACCCCTGGGCAAGCTTCTCTGAG	1764
QY	461	ProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArgLysAlaAla	480
DB	1765	CCAGGACGCTGCTATGAGGAGCTTCTCAAGTACTTGGTGTATACATCTTCCGAAGACGCC	1824
QY	481	ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPro	500
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QY	501	ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg	520
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QY	601	GlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys	620
DB	2185	CAGGACCCCTTCCAGATGCCCATCGGAGGATCTGTGGTAGGACTGTGGTAGGAGGAG	2244
QY	621	ValTyrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuVal	640
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QY	661	PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys	680
DB	2365	TTGAGTCCATGACCAAGCTTCTTGGAGACACAGAGTACGGGAGCTGCCATAGCTCTCTGC	2424
QY	681	LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro	700
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4705	Db	GGGTGCAGCTCTTCAAAGGAAGTTCTTCGTGTGTACGGGTGAGACACCAAGAACATC	4764
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AUTHORS	McRory, J.E., Santi, C.M., Hamming, K.S., Mezeyova, J., Sutton, K.G., Baillie, D.L., Stea, A. and Snutch, T.P.		
TITLE	Molecular and functional characterization of a family of rat brain T-type calcium channels		
JOURNAL	J. Biol. Chem. 276 (6), 3999-4011 (2001)		
MEDLINE	21264893		
PUBMED	11073957		
REFERENCE	2 (bases 1 to 6942)		
AUTHORS	Snutch, T.P., McRory, J.E. and Hamming, K.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-JUL-2000) Biotechnology Laboratory, University of British Columbia, 6174 University Blvd., Vancouver, BC V6T1Z3, Canada		
REFERENCE	3 (bases 1 to 6942)		
AUTHORS	Snutch, T.P., McRory, J.E. and Hamming, K.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-NOV-2000) Biotechnology Laboratory, University of British Columbia, 6174 University Blvd., Vancouver, BC V6T1Z3, Canada		
REMARK	Sequence update by submitter		
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RESULT 3
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DEFINITION alpha subunit (CACNA1G) mRNA, complete cds.
ACCESSION AF027984
VERSION AF027984.1 GI:3786350
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 7542)
Perez-Reyes, E., Cribbs, L.L., Daud, A., Lacerda, A.E., Barclay, J.,
Williamson, M.P., Fox, M., Rees, M. and Lee, J.H.
Molecular characterization of a neuronal low-voltage-activated
T-type calcium channel.
NATURE 391 (6670), 896-900 (1998)
98154730
9495342

2 (bases 1 to 7542)
Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.
Direct Submission
Submitted (02-OCT-1997) Physiology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
3 (bases 1 to 7542)
Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.
Direct Submission
Submitted (22-OCT-1998) Physiology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
SEQUENCE update by submitter
On Oct 24, 1998 this sequence version replaced gi:2921748.
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ORIGIN

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Db	5365	TCAAACTTGTGGCTTTGGCTTCGCGCTTCTTCCAGACAGGTGGAACACAGCTGGACC	5424	Db	6445	CTGGGGCGCATCTCCTAACTACCCCACTGGCGCTCCCTCTGGCTCAGAGGCGTC	6504
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				VERSION			
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				GI:33033849			
				JP 2002525077-A/2.			
				KEYWORDS			
				Rattus sp.			
				ORGANISM			
				Rattus sp.			
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
				Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
				Rattus.			
				REFERENCE			
				1 (bases 1 to 7285)			

BD224079 7285 bp DNA linear PAT 17-JUL-2003

T-type calcium channel.

BD224079

BD224079.1 GI:33033849

JP 2002525077-A/2.

Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 7285)

AUTHORS Li.M.
 TITLE T-type calcium channel
 JOURNAL Patent: JP 2002525077-A 2 13-AUG-2002;
 SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION
 COMMENT OS Rattus sp. (rat)
 PN JP 2002525077-A/2
 PD 13-AUG-2002
 PF 26-AUG-1999 JP 2000570372
 PR 26-AUG-1998 US 60/098004,27-JAN-1999 US 60/117399 FI
 MING LI
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 C07K16/18,
 PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/68,G01N33/
 PC 15,G01N33/50,
 PC G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/58// PC
 C12P21/08,
 PC C12N15/00,C12N5/00
 CC T-type calcium channel
 FH Key Location/Qualifiers
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 FT /organism='Rattus sp. (rat)'.
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 /organism='Rattus sp.'
 /mol_type='genomic DNA'
 /db_xref='taxon:10118'
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 Score: 11829.00 Matches: 2270
 Percent Similarity: 97.72% Conservative: 1
 Best Local Similarity: 97.68% Mismatches: 15
 Query Match: 98.35% Indels: 38
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 QY 20 rgProSerSerAspProGlyProArgLeuAlaArgGlyTyrThrArgArgMetG 40
 DB 117 GCCCTCTTCGACCCCGGGGCGCGGTCGGCCAGAGATGACGAGGAGGAGATGG 176
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Db	2577	CTACAACATCTTGATGTGTCAATGTGGTCATCAGTGTGGAGATTTGGGCCAGCA	2636
QY	859	nglyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr	879
Db	2637	GGGAGGTGGCTGTGGTGTGCGGACCTTCCGCTGTATGCGGTGTGTGAAGCTGTGCG	2696
QY	879	gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl	899
Db	2697	CTTCTCGCCGCCCTGCAGCCAGCTCGTGGTGTCTATGAAGACCATGGCAACAGTGGC	2756

QY	899	aThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisle	919
Db	2757	CACCTTCTTCGATGCTCCTCATGCTGTTTCATCTTATCTTACGATCCTTGGCATCACT	2816
QY	919	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	2817	CTTTGTTTGAAGTTTCGCATCTGAACGGGATGGGACACGTTGCCAGACCCGGAAGATTT	2876
QY	939	eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs	959
Db	2877	CGACTCCCTGCTCTGGGCATCGTCACTGTCTTTCAGATTTGACTCAGGAAGACTGGAA	2936
QY	959	nLysValLeuTyAsnGlyMetAlaSerThrSerTrpAlaAlaLeuTyPheIleAl	979
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Db	2997	CCTCATGACTTTTGGCAACTATGTCTTTAACTGCTGGTGGCAATCTTCTTGTGGAGG	3056
QY	999	yPheGlnAlaGlu-----	1003
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QY	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePh	1016
Db	3117	GCTGCTGTCACTCTCAGGGGGAGATGCCACCAAGTCTGAGTCAGAGCTGATTTCTT	3176
QY	1016	eSerProSerValAspGlyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGl	1036
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QY	1036	yGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaTh	1056
Db	3237	AGAACACGCGGAACCTACGAAAGAGCTTTTGCCACCCCTCATCATCCATCCGCTGGAC	3296
QY	1056	rProMetSerHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySe	1076
Db	3297	ACCAATGTCTACTACCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACCTGGGCTCTGGCTC	3356
QY	1076	rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy	1096
Db	3357	TCGACGTACACAGTAGCGGTGGCTGAGCTGGAGTGGCCCATGAGATGAAATC	3416
QY	1096	sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1116
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QY	1116	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe	1136
Db	3477	CAGCGCTCCAGCAGGAACAGGCTTGGGCCGGGCCCCAGCCTAAACGGAGGAGCCCGAG	3536
QY	1136	rglyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGlnAspGluGluGluse	1156
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QY	1156	rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGl	1176
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QY	1176	uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr	1196
Db	3657	ACGTGAGGCCAAGAGTTCTTTGACCTGTGACCTCTGCAGGTGCCGGGGTGCACCG	3716
QY	1196	gThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSe	1216
Db	3717	CACAGCCGCGCGGAGCTCTGCTCTGAGCACCAGAGCTGTAAATGGCAAGTCGGCTTC	3776
QY	1216	rGlyArgLeuAlaArgThrLeuArgThrAspProGlnLeuAspGlyAspAspAs	1236
Db	3777	AGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCACTGATGGGATGATGACAA	3836
QY	1236	nAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPr	1256

Db		3837	TGATAGGGAATCTGAGCAAGGGGAAAGCATACAAAGCCTGGGTGAGATCCCGGCTTCC	3896		4917	GTCAAGAGCCAGTCGCAAGCCCTACTACTCTCGAGATTCGGGCTCTTGTCCA	4976
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Qy	aGluArgIlePheLeuThrIleuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMe	1316		1336		1665	eAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLe	1685
Db	TGAGCGCATCTTCTGACCTCTCCAACTACATCTTTCAGCGAGCTCTTCTAGCTGAAT	4077		4136		5157	TGGCTTCCGCGCTTCTTTCAGGACAGTGTGAACAGCTGGACTGGCTGTCTTGTGCTTCT	5216
Qy	tThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSe	1336		1356		1685	uSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnPr	1705
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Db	CACACAGAAACATCACTAACAAATCCGACTGGCTGAGCCAGCTACCGATGGGTCCGGA	4497		4556		5577	TGGAATTATGAAGACACCCCTCGGGACTGTGACACAGAGTCCACCTGTACACACTGT	5636
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Db	CATCATGAACCAACCCCTGGATGCTGTATATCTTCTCTCTCTCTCTCTCTCTCTCTCT	4677		4736		5757	CGAGCTCGAGCCGAGCTGGAGCTGGAGATGAAGAGCTCAGCCCGCAGCCCCACTCCCC	5816
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Db	CTTCTTGTCTGAACATGTTTGTGGCGGTGTGTGGTGGAGAACTTCCATAAGTCAGACA	4737		4796		5817	GCTGGGAGCCCTTCTCTGGCCCGGGGTGGAGGGTGTCAACAGATCCTGACAGCCCTAA	5876
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Qy	sLysArgArg-----SerLysGluLysGlnMe	1585		1585		1925	sProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh	1945
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Db	-----	1605		1605		5997	TGTGAGGAAGTCTGGTGTGAGCGGAGCGACTCTCTGCCCCAATGACAGCTACATGTGCCG	6056

QY	1965	gAnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProGlyAlaG1	1985
Db	6057	CAATGGAGCACTGCTGAGAGATCCCTAGGACACAGGGCTGGGGCTCCCAAGCCCA	6116
QY	1985	nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleIleuGlnIle	2005
Db	6117	GTGAGGCTCCATCTTGTGCTTCCACCAACAGCAGACACAGCTGATCTTACAGCT	6176
QY	2005	uProLysAspValHisTrpLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePr	2025
Db	6177	TCCCAAGATGTCATATCTGTCAGGCTATGCGGGCCCCACCTGGGGCCCATCCC	6236
QY	2025	oLysLeuProProGlyArgSerProLeuAlaGlnAArgProLeuArgArgGlnAlaAl	2045
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Db	6297	AATAAGGACTGACTCCCTGATGTGAGGCGCTGGGTAGCCGGAAGACTGTTGTGAGA	6356
QY	2065	uValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerI1	2085
Db	6357	GGTGAGTGGCCCTCTGCGCTCTGACCGGTCTCTATCTTCTGGGGGGTCCGAGCAT	6416
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Db	6777	GGGTCTGGGAGCGGCTTGAAGAAACCTCAGCCCAACCTCAGATCTCTATAGACCCCC	6836
QY	2225	oGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaPr	2245
Db	6837	GGAGGACAGGCTCTCGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6896
QY	2245	oAlaSerAspSerLysAspProSerValSerProLeuAspSerThrAlaAlaSerPr	2265
Db	6897	GGCCAGTGACTCTAAGGATCCCTCGGCTCTCAGCCCTCTTACAGCAGCGGCTGCTCAC	6956
QY	2265	oSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAs	2285
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RESULT 5
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LOCUS
DEFINITION Rattus norvegicus T-type calcium channel isoform mRNA, linear ROD 19-OCT-2001

ACCESSION AF125161
VERSION AF125161.1
KEYWORDS GI:4633669
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 7286)
AUTHORS Zhuang,H., Bhattacharjee,A., Hu,F., Zhang,M., Goswami,T., Wang,L.,
Wu,S., Berggren,P.O. and Li,M.
TITLE Cloning of a T-type Ca2+ channel isoform in insulin-secreting cells
JOURNAL Diabetes 49 (1), 59-64 (2000)
MEDLINE 20081696
PUBMED 10615950
REFERENCE 2 (bases 1 to 7286)
AUTHORS Zhuang,H., Hu,F., Bhattacharjee,A., Zhang,M., Wu,S., Berggren,P.
and Li,M.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-1999) Pharmacology, University of South Alabama,
Mobile, AL 36608, USA
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 7286)
Zhuang,H., Bhattacharjee,A., Hu,F., Zhang,M., Goswami,T., Wang,L.,
Wu,S., Berggren,P.O. and Li,M.
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20081696
10615950
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Zhuang,H., Hu,F., Bhattacharjee,A., Zhang,M., Wu,S., Berggren,P.
and Li,M.
Direct Submission
Submitted (01-FEB-1999) Pharmacology, University of South Alabama,
Mobile, AL 36608, USA
Location/Qualifiers
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ORIGIN

Alignment Scores:

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 Percent Similarity: 97.72% Conservativeness: 1
 Best Local Similarity: 97.68% Mismatches: 15
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US-09-611-257A-24 (1-2287) x AF125161 (1-7286)

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Db	298	GGCGAGGGGTCGCGTACCGGGCGCTAGCCCGGGTGTCTTCTTCTTCTTCTTCTTCT	357
Qy	99	pSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValSe	119
Db	358	CAGCGCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAAACCGGTGGTTCGAGCGAGTCAG	417
Qy	119	rMetLeuValileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspII	139
Db	418	TATGCTGGTCACTTCTCAACTGTGTACTCTGGGTATGTTTTCAGGCGGTGTGAGGACAT	477
Qy	139	eAlaCysAspSerClnArgCysArgIIleLeuGlnAlaPheAspPheilePheAlaph	159
Db	478	TGCTGTGACTCCAGCGCTGCGGATCCCTGACGGCTTCGATGACTTCATCTTTGCTTT	537
Qy	159	ePheAlaValGluMetValIlysMetValAlaLeuGlyIlePheGlyIlysCysTy	179
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Qy	179	rLeuGlyAspThrTrpAsnArgLeuAspPhePheileValileAlaGlyMetLeuGluTy	199
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Qy	199	rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr	219
Db	658	TTGCTGGACCTGCAGAACGTCAGCTTCTCCGACGTCCAGACAGTCCGCTGTGTCGACC	717
Qy	219	oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh	239
Db	718	GCTCAGGGCCATTTAACCGGGTGCCACGATGCGCATTTCTGTCACATTTCTTGGACAC	777
Qy	239	rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheilePheGlyII	259
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Qy	259	eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh	279
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Db	898	CAGCTCCCTGAGCGTGACCTGGAGCCTTATTACCAGACAGAAATGAGGACGAG	957
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Db	958	CCCTTTTCATCTGCTCTCAGCCTCGGGAATGGCATGAGATCTCTGCAAGGAGTGTGCCAC	1017
Qy	319	rLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAnSe	339
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Db	1078	TTCCAGCAACACCACTGTGTCAACTGGAACACGATCTATACCAACTGCTCTCGGGCGGA	1137
Qy	359	uHisAsnProPheIysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaII	379
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Qy	379	ePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHi	399
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Db	1318	CAACCTGTGCTGGTGTGATTCGACGCGATTTCTCGAGACCAACAGCGGGAGAGTCA	1377
Qy	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
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Qy	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499
Db	1498	AGCCCGAAGCTGGCCCGAGGTCTTAGGGCTATAGGGCTGCGGGCTGGGTCTCAGCAG	1557
Qy	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519
Db	1558	CCAGTGGCCCGTAGTGGGAGGAGCCCGAGCCAGTGGCAGCTGCTGCTCAGACCG	1617
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Qy	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559
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LOCUS BD224078 7129 bp DNA linear PAT 17-JUL-2003
DEFINITION T-type calcium channel.
ACCESSION BD224078
VERSION BD224078.1 GI:33033848
KEYWORDS JP 2002525077-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Li, M.
T-type calcium channel
Patent: JP 2002525077-A 1 13-AUG-2002;
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OS Rattus sp. (rat)
PN JP 2002525077-A/1
PD 13-AUG-2002
PF 26-AUG-1999 JP 2000570372
PR 26-AUG-1998 US 60/098004, 27-JAN-1999 US 60/117399 PI
MING LI
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CC T-type calcium channel
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US-09-611-257A-24 (1-2287) x MMU012569 (1-7625)

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1869	Db	GAAGGTATACCCCACTGTGCATACCAGCCCTCCACACAGAGTCTGAAGGATTAAGCACT	1928	
639	QY	uValGluVal	AlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGI	659
1929	Db	AGTGGAGGTGGCCCCCAGCCCTGGGGCCCCCACCCTCACCACTTCAACATCCACCCTGG	1988	
659	QY	yProPheSer	SerMethHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe	679
1989	Db	GCCTTTCAGTCTCCATGCACAAGTCTCTGGAGACACAGATACGGAGCCCTGCCATAGCTC	2048	
679	QY	rCysLysIle	SerSerProCysSerLysAlaAspSerGlyValaCysGlyProAspSerCy	699
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699	QY	sProTyrCys	AlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs	719
2109	Db	TCCCTACTGTGCCCGGACGAGCAGGGAGCCAGAGTCCCGTGCACCATGAAATGCCTGA	2168	
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2169	Db	CTCAGACAGTGAAGCTGTGTATGAGTTTCACACAGGAGCGCTCAGCACAGCACTCCGGGA	2228	
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2229	Db	TCCCCAC---AGACGGCGAGCGCGGCGCCCTGGGGCCCCAGATCGACAGCGCTAGTTCTGTGCT	2285	
759	QY	uAlaPheTrp	ArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGI	779

Db	2286	GGCCTTCTGGAGGCTGATCTGCGACACATTC	CGGAAGATCGTAGATAGCAAAATAC	TTTGG	2343
Qy	779	YArGgIyIleWetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluYrHisG		799	
Db	2346	CCGGGAATCATGATCGTATCTCTGGTCAATAC	CCCTCAGCATGGGCATCAGGTACCA	CGA	2405
Qy	799	uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPhe		819	
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Qy	819	eAlaLeuGluWetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnPr		839	
Db	2466	CGCCTTGGAGATGCTGCTGAAGCTGCTGCTG	TACGGTCCCTTCGGCTACATTAAGAAATCC		2525
Qy	839	oTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnG		859	
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Qy	999	yPheGlnAlaGlu-----	-----	1003	
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Qy	1004	-----	-----GlyAspAlaThrLysSerGluSerGluProAspPhePh		1016
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1176 uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr 1196
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1718 gValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGl 1738
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[illegible]

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Db	6726	AAG	CTCGGGGGCCAACTCTTGGGGCCCTGGAGCCGGCTTAAGAAAACTCAGCCC	6785
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Db	6786	ACC	CAGTATCTCTATAGACCCCGGAGACCCAGGGCCCTCGGCCCCCATGCAATCTCTGG	6845
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RESULT 8				
LOCUS	BC057399		7527 bp	mrna
DEFINITION	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit, mRNA (cDNA clone MGC:62312 IMAGE:6410519), complete cds.			
ACCESSION	BC057399			
VERSION	BC057399.1		GI:34783700	
KEYWORDS	MGC.			
SOURCE	Mus musculus			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 7527)			
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunatathne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerker, A., Schein, J.E., Jones, S.J. and Marra, M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
MEDLINE	2388257			
PUBMED	12477932			
REFERENCE	2 (bases 1 to 7527)			
AUTHORS	Strausberg, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NTH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cqabs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa cDNA Library Arrayed by: The I.M.A.G.E. Consortium (fLNU) DNA sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305			

Web site:	http://www-shgc.stanford.edu		
	Contact: (Dickson, Mark) mcd@paxil.stanford.edu		
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINU at: http://image.llnl.gov		
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US-09-611-257A-24 (1-2287) x BC057399 (1-7527)

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QY 459 rGluProGlySerCysTyrlGluGluLeuLysTyrlLeuValTyrlleLeuArgLysAl 479
DB 1650 TGAGCCAGGACGCTGCTATGAGGAGCTTCTCAAGTACTTGGTGTACATCTCTCCGCAAGC 1709
QY 479 aAlaArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499
DB 1710 AGCCCGCAGGCTGGCCAGGCTCTAGGGCTGTAGGCGTGGCGGCTGGGTGTCTCAGCAG 1769
QY 499 rProValAlaArgSerClyGlnGluProGlnProSerGlySerCysThrArgSerHisAr 519
DB 1770 CCAGTGGTCCGCGGGGAGAGCCCGAGCCAGTGGCGAGTGTCTCTGTTCCACACCG 1829
QY 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisLe 539
DB 1830 TCGTCTGTCTGCCACCACTGCTGTCACCACTATCACCACCACTACCACTACCACT 1889
QY 539 uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559
DB 1890 GGGTAATGGACGCTCAGAGTTCCTCCGGGCGAGCCAGAGATCCAGACAGGATGCCAA 1949
QY 559 nGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGlyProPr 579
DB 1950 TGGGTCCGCTGGCTCATGCTGCCACCCCTTACCCCCACCTCTCTGGGGGCCCTCC 2009
QY 579 oArgGlyAlaGluSerValHisSerPheTyrlHisAlaAspCysHisLeuGluProValAr 599
DB 2010 GAGGGTGGAGTCTGTACAGCTTCTACCATGCTGACTGCACCTTGGAGGCGAGTCCG 2069
QY 599 gCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGI 619
DB 2070 TTCCAGGGCGCCCTCCAGGTCCCATCGAGGATCTCGGAGGATCTGGGAGTGTGG 2129
QY 619 yLysValTyrlProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe 639
DB 2130 GAAGGTATACCCCACTGTGCATACAGCCCTCCAGGAGATGCTGAAGGATGAAGGACT 2189
QY 639 uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGI 659
DB 2190 AGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACCAGCTTCAACATCCACCTGG 2249
QY 659 yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe 679
DB 2250 GCCCTTCAGCTCCATGCACAAGCTCTCTGGAGACACAGAGTACGGAGCCCTGCCATGCTC 2309
QY 679 rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy 699
DB 2310 CTGCAAAATCTCCAGCCCTTGTCTCCAAAGGACAGTGGAGGCTGTGGGCGGACAGTTG 2369

699 sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs 719
Db TCCCTACTGTGCCGACAGGAGCAGGGAGCCAGAGTCCGCTGACCATGAATGCTGA 2429
719 pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs 739
Db CTGAGACAGTGGCTGTGTATGAGTTCACACAGGACGCTCAGCACAGCGACCTCCGGGA 2489
739 pProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle 759
Db TCCCCAC---AGACGGCGACGGCGAGCCTGGGCCAGATGACAGACCTAGTTCGTGCT 2546
759 uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG 779
Db GGCCTTCTGGAGGCTGATCTGCGACACATTCGGAAGATCGTAGATAGCAATACTTTGG 2606
779 yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisG 799
Db CCGGGGAATCATGATCGCTATCTGCTCAATACCTCAGCATGGGCATCGAGTACCAGCA 2666
799 uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh 819
Db GACGCCGAGGAGCTCACCAAGCCCTGGAAATCAGCAACATCGTCTTACCAGCCCTCTT 2726
819 eAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnPr 839
Db CGCCTTGGAGATGCTGCTGNAGCTGCTGCTACGGTCCCTTCGGCTACATTAAGATCC 2786
839 oTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnG 859
Db CTACAACATCTTTGATGGCGTCAATTGTGTTCATCAGCGTGTGGGATTTGTGGCCAGCA 2846
859 nGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr 879
Db GGGAGTGGCCCTGTCGGTGTGGGACCTTCGCCCTGATCGCGGTGCTGAAGCTAGTTCCG 2906
879 gPheLeuProAlaLeuGlnArgGlnValValLeuMetLysThrMetAspAsnValAl 899
Db CTTCCTGCCGCACTGCAGCGGAGCTCGTGTGCTCATGAACCATGGACACAGCTGGC 2966
899 aThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLe 919
Db CACCTTCTGATGCTGCTATGCTCTTCATCTTCATCTTCAGCATCTGGGCATGCACCT 3026
919 uPheGlyCysLysPheAlaSerCluArgAspGlyAspThrLeuProAspArgLysAsnPh 939
Db TTTTGTTCGAAGTTCGCAATCTGAACGGGATGGGACACGTTGCCAGACCGGAAGAATTT 3086
939 eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs 959
Db TGNACTCCCTGCTCTGGGCCATTGTCACTGTCTTTTCAGATTCGACTCAGGAGACTGGAA 3146
959 nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl 979
Db TAAAGTCCTTTACAACGGCATGGCTCCACGTCACTCTGGCTGCTCTTTACTTTCATCGC 3206
979 aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999
Db CCTCATGACTTTTGGCAACTACGTGCTCTTTAACCTGCTGTGCGCATTCCTGTGGAGGG 3266
999 yPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSe 1019
Db TTTCCAGGACAGGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTCGCCAG 3326
1019 rValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyLysHisAl 1039
Db TGTGATGTGTGATGGGACAGGAAGAAGCGCTTGGCCCTTGGTGGCTTGGGAGAACACTC 3386
1039 aGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetSe 1059
Db GGAACATACGAAGAGCCTTTTGGCACCTCTCATCATCCACACAGCTGCATACCGATGC 3446
1059 rHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgTh 1079

3447 ACTGCCCAAGAGCTCCAGCACAGGTGTGGGGAAAGCACTGGGCTCTGGGCTCTCGCCGCAC 3506
QY rSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSe 1099
Db CAGTAGCAGTGGTCCGCTGAGCCTGGAACTGCTCATCATGAGATGAATACCCGCAAG 3566
1099 rAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSe 1119
Db TCCCCGAGCTCCCCGACAGTCCCTGGAGCCGACGACGACGACTGGACACGAGGGCGCTC 3626
1119 rSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluAr 1139
Db CAGCCGGAACACCTGGGCGCGGCCAGCTGAAGCGTAGGAGCCCAAGCGGGAGCG 3686
1139 gArgSerLeuLeuSerGlyGluGlyGlnSerGlnAspGluGluGluSerSerGluGl 1159
Db GAGGTCCCTGCTGCTGGAGAGGCTCAGGAGAGCCAGGATGAGGAGGAGAGTTCAAGAAG 3746
1159 uAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAl 1179
Db GGACCGGGCCAGCCAGCAGGAGGATCATCCGACAGGGGTTCCTTGGAACTGTGAGGC 3806
1179 aLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSe 1199
Db CAAGAGTTCTTTGACCTGCTGACACCTGCGAGTGGCCCGGCTTCATCGAACAGCCAG 3866
1199 rGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLe 1219
Db CGGTGGAGCTGCTGCTCTGAAACACCAAGACTGTAATGGCAAGTCCGCTTCAGGGCGTTT 3926
1219 uAlaArgThrLeuArgThrAspProGlnLeuAspGlyAspAspAsnAspGluGl 1239
Db GGGCCGACCTTGGCGGTGATGACCCCCACTGATGGGGATGATGGCGATGATGAGGG 3986
1239 yAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCy 1259
Db CAACTGTAGCAAGGGAACGCTTACGAGCCTGGGTCCGAGCCCGGCTCCCTGCCTGTG 4046
1259 sArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLe 1279
Db CCGAGAGCGAGATTCCTGGTCTGCTATATCTTCCTCCCTCCCAAGTCAAGGTTTCGTCT 4106
1279 uCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLe 1299
Db GGTACCCGATCATCACCACAGATGTTTGACCATGTGGTCTCTCTCATCATCTCTCT 4166
1299 uAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI 1319
Db CAACTGTATCACCATCGCTATGGAGCGGCCCAAAATTTGACCCCAAGCGCTGAACGCAT 4226
1319 ePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVally 1339
Db CTTCTCGACCTCTCCAACATACATCTTCACGCGAGCTTTCCTGGCTGAAATGACAGTGA 4286
1339 sValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnVa 1359
Db GGTGTGGACATGGGCTGGTGTGTTTGGGAGCAGGCCCTACCTCGCGAGCAGCTGGNACGT 4346
1359 lLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAs 1379
Db GCTGGAGCGGCTGCTGGTGTCTCATCTGTATGCACATCTCTGGTGTCTCATCTCTCTGA 4406
1379 pSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPr 1399
Db CAGCGGCACCAAGATTCGGCATCTGAGGTGTGGGGCTGCTGGGCTGCTGCGACCTACGTCC 4466
1399 oLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSe 1419
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1419 rLeuLysProIleGlyAsnIleValIleCysAlaPhePheIleIlePheGlyI 1439

Db 4527 CCTCAAAACCCATTGGCAACATTTGGTTCATCTGCTGCTCTCTTCATCATTTTTTGGAAAT 4586
Qy eLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyClnuAspThrArgAs 1459
Db TCTTGGGGTGGAGCTCTTCAAAAGGAAGTTCTTCGTGTGTCAGGGTGAGGACCAAGGAA 4646
Qy nileThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAs 1479
Db CATCACTAAACAGTCCAGCTGTGTGAGGCCAGTTACCGGTGGTCCGGCACAAGTACAA 4706
Qy nPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyr 1499
Db CTTTGACAACCTGGCCAGGCTCTGATCTCCCTTTGTGCTGGCCCTCCAAGGATGGCTG 4766
Qy pValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAs 1519
Db GGTTGACATCATGATGATGAGCTGGAGTGTGTGGAGTGGACAGAGCCCATCATGAA 4826
Qy nHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheVa 1539
Db CCACAACCCCTGGATGCTCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4886
Qy lLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnG 1559
Db CTTGAACATCTTTGTGGCGCTGGTGGTGGAGAACTTCCATAAGTGCAGGCGAGCACCAGGA 4946
Qy uGluGluAlaArgArgArgGluLysArgLeuArgLeuGluLysLysArgAr 1579
Db GGAGGAGGAGCGCGCGCGGAGGAGAAAGCGACTAAAGAGGCTGGAGAAAGAGAAAG 5006
Qy g-----SerLysLysLysGlnMetAlaGluAl 1588
Db GAATCTAATGTTGACGATGTAATGCTTCGGGAGCTCAGCCAGCGCTCGCTCAGAGAC 5066
Qy aGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCy 1608
Db CCAGTGCAAACCCCTACTACTCTGACTACTCGGCTTCGGCTTCCTCGTCCACCACTGTG 5126
Qy sThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMe 1628
Db TACCAGCCACTACTGACCTCTTCATCACTGGTGTCTCGGGCTGAATGTGTGCAGAT 5186
Qy tAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTy 1648
Db GGCCATCGAACATTTACCAGCAGCCCGAGATCTCGGACAGGCTCTGAAGATCTGCAACTA 5246
Qy rIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheAr 1668
Db CATCTTTACCGTCATCTTTGTCTGGAGTCAGTATTCAAACCTTGTGGCCCTTCGGCTTCG 5306
Qy ArgPheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMe 1688
Db CCGGTCTCTCCAGGACAGGTGGAAACAGCTGGACCTGGCTATTGTGTCTCTGTCATCAT 5366
Qy tGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIl 1708
Db GGGCATCCAGCTCGGAAGATTTAGGTCATATGCTTCACTGCCCATCAACCCCACTCAT 5426
Qy eArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValG 1728
Db CCGTATCATGAGGGTCTCCGCTTGTCTGAGTTCTGAAGTCTTGAAGATGGCTGTGGG 5486
Qy MetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLe 1748
Db CATCGGGGCACTGCTGGACACGGTGTATGCAAGCCCTGCCAGGTGGGGAACTTGGGACT 5546
Qy uLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLe 1768
Db TCTCTTCATGCTATATTTTTCATCTTTTGACGCTCTCGGCGTGGAGCTCTTTGAGACCT 5606
Qy uGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPh 1788
Db GGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGGGCGGCGCATGCCACCTTTAGAACTT 5666

Qy eGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGlyIleMe 1808
Db TGGTATGGCCCTTTCTGACCCCTCTTCGAGTCTCACTGGTGACACTGGATGGTATTAT 5726
Qy tLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerPr 1828
Db GAAGGACACCCCTCCGGGACTGTGACAGGAGTCCACCTGTACAACACCGCTCATCTCAC 5786
Qy oIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAl 1848
Db CATCTACTTCTGCTCTCTGCTGACGGCCAGTTTGTCTCAACCTGGTGCATAGC 5846
Qy aValLeuMetLysHisLeuGluSerAsnLysGluAlaLysGluGluAlaGluLeuG 1868
Db CGTCTGTATGAACACCTGGAAGAGAGCAACAAGAGGCCCAAGAGGAGCGGAGTTGGA 5906
Qy uAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySe 1888
Db GCGGAGCTGGAGCTAGAGATGAAGACACTCAGCCCGCAGCCCACTCCCGCTGGGCAG 5966
Qy rProPheLeuTyrProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAl 1908
Db CCCCTTCTCTGCGCTGGGTGGAGGTGTCAATAGCCCTGACAGCCCTTAAGCCTGGGC 6026
Qy aProHisThrThrAlaHisIleGlyAlaAla---SerGlyPheSerLeuGluHisProTh 1927
Db TCCACACACCCAGGCCCCACATTTGGAGCAGCTCTTCAAGGCTTCTCCCTTGAGCACCCAC 6086
Qy rMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrValAr 1947
Db GATGTTACCTCACACTGAGGAGGGCCAGTCCCTTAGGACAGACCTGTGCTGAGTGTAG 6146
Qy gLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnG 1967
Db GAAAGTCTGGTGTGAGCGGACACACTCTCTGCCCAATGACAGCTACATGTGCCCAATGG 6206
Qy ySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerG 1987
Db GAGCATCTGCCAGAGATCCCTTAGGACACAGGGGCTGGGGCTCCCCAAGAGCCAGTCAGG 6266
Qy ySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLy 2007
Db CTCATCTTGTCTGTTTCACTCCCAACAGCAGACACAGCTGCATCTCATAGCTTCCCAA 6326
Qy sAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTyrPcIlyAlaIleProLysLe 2027
Db AGATGCACACTATCTGCTCCAGCTCATGGGGCTTCCACCTGGGGGCCCATCCCTAAACT 6386
Qy uProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaIleAlaIleAr 2047
Db ACCCCACCTTGGCGCTTCCCTCTGGCTAGAGGCTCTCAGGGCCAGCAGCAATAG 6446
Qy gThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluValSe 2067
Db GACTGACTCCCTGAGCTGAGGCTGGCTGGGTAGCCGGAGAGACCTGTTGTGACAGGTGAG 6506
Qy rGlyProSerCysProLeuThrArgSerSerSerPheThrPcIlyGlySerSerIleGlnVa 2087
Db TGGGCGCTCTGCGCTCTGACCCGCTCTCATCTCTTCTGGGGGGGTGCGAGCATCCAGGT 6566
Qy lGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCy 2107
Db GCAGCAGCGCTCCGGCAGCCAGCAAAAGTCTCAAGACATCTCCCTTCCAGGCCCTTGG 6626
Qy sProGlyLeuGluProSerTyrAlaLysAspProProGluThrArgSerSerLeuGluLe 2127
Db CCCAGGCTCGAAACCCAGCTGGGCCAAGGACCTCAAGAGACAGAGAGCTTAGAGCT 6686
Qy uAspThrGluLeuSerTyrPheSerGlyAspLeuLeuProSerSerGlnGluProLe 2147
Db GGACCGGAGCTGAGCTGGATTTTTCAGGAGACCTCTCTGCCAGCAGTCCAGGAACCCCT 6746

444	Db	TCATCCTTCTCAACTGCGTGACCTCGGGCATGTGTTCCGGCCATCGCAGGACATCGCCTGTG	503
142	Qy	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaVal	162
504	Db	ACTCCACGCGCTGCCGATCCTGCGAGCCTTTGATGACTTTCATCTTTGCCCTTCTTTCCGCG	563
162	Qy	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA	182
564	Db	TGGAGATGGTGGTGAAGATGGTGCCCTTGGGCATCTTTTGGGAAAAAGTGTTACTCGGGAG	623
182	Qy	spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA	202
624	Db	ACACTTGGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGAGTCTCGAGTACTCGCTGG	683
202	Qy	spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
684	Db	ACCTGCAGAACGTCAGCTTCTCAGCTGTCAGGACAGTCCGCTGTGTCGACCGCTCAGGG	743
222	Qy	lalleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM	242
744	Db	CCATTAAACCGGGTGCCACGATCGGCATCTCTGTGTACGTTCGTGTCGTACGCTGCCA	803
242	Qy	etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV	262
804	Db	TGCTGGGCAACGTCCTGCTGCTCTGCTTCTTCGTCTTCTTCATCTTCGGCATCGTCGGCG	863
262	Qy	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP	282
864	Db	TCCAGCTGTGGCAGGGCTGCTTCGGAAACGATGCTTCTTACCTGAGAAATTCAGCCTCC	923
282	Qy	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI	302
924	Db	CCCTGAGCTGGACCTCGAGCGCTATTACACAGACAGAGAACGAGGATGAGAGCCCTTCA	983
302	Qy	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
984	Db	TCGTCTCCCAAGCCACGCGAGAACGGCATGGCTCCTCGAAGCGTGCCACGCTGCGCG	1043
322	Qy	lyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerA	342
1044	Db	GGGACGGGGCGGTGGCCACCTTGGCGTCTGGACTATGAGGCCCTACAACAGCTCCAGCA	1103
342	Qy	snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP	362
1104	Db	ACACCCTGTGTCAACTGGAAACAGTACTACACCAACTGCTCAGCGGGGAGCACAAACC	1163
362	Qy	roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV	382
1164	Db	CTTTCAGGGCGCCCATCAACTTTTGACAAACATTTGGCTATGGCTATGGCATCTTCCAGG	1223
382	Qy	alIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
1224	Db	TCATCAGCTGGAGGCTGGGTGCACATCATGTACTTTTGTGATGGATGCTCATTTCTTCT	1283
402	Qy	yrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuC	422
1284	Db	ACAATTTTCATCTTTCATCTCCTCATCATCGTGGGCTCCTTCTTTCATGATCAACCTGT	1343
422	Qy	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
1344	Db	GCCTGGTGGTGATTGCCACGAGTTCTCAGACCAAGCAGCGGGAAGCCAGCTGATGC	1403
442	Qy	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
1404	Db	GGGAGCAGCGTGTGCGGTTTCTGTCCAAGCCAGCACCTGTGGCTAGCTTCTTGAGCCCG	1463
462	Qy	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
1464	Db	GCAGCTGCTATAGGAGCTGCTCAAGTACCTGGTGTATCATCTTCTGTAAAGCAGCCCGCA	1523
482	Qy	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
1524	Db	GGCTGGCTCAGGTCCTCTCGGCGACAGGCTGTGCGGGTTGGGCTGCTCAGCAGCCAGCAC	1583

Qy	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1584	CCCTCGGGGCCAGAGAGACCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCGCCTAT	1643
Qy	522	erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHis	542
Db	1644	CCGTCCACCACTTGGTGACACACACACACACCATCACCACTACCACTCGGCANTG	1703
Qy	542	lyThrLeuArgValProArgAlaSerProGluLeuGlnAspArgAspAlaAsnGlySerA	562
Db	1704	GGACGCTCAGGGCCCCCGGGCCAGCCCGAGATCCAGACAGGATGCCAATGGGTCCC	1763
Qy	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1764	GCCGGTCTATGCTGCGCACACACACCCCTCCAGCGCTGCCCTCTCCGGGGCCCCCT	1823
Qy	582	laGluSerValHisSerPheThrHisAlaAspCysHisHisLeuGluProValArgCysGlnA	602
Db	1824	CAGAGTCTGTGCACAGCTTCTACCATCGGACTGCGCATTTAGAGCCAGTCCGCTGCCAGG	1883
Qy	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	1884	CGCCCCCTCCAGGTCCCCATCTAGGCATCCCGCAGGACTGTGGGCAGCGGGAGGTGT	1943
Qy	622	yrProThrValHisThrSerProProGluLeuLeuLysAspLysAlaLeuValGluV	642
Db	1944	ATCCACCGGTGCACACAGCCCTCCACCGAGACGCTGAAGGAGAGGCACTAGTAGAGG	2003
Qy	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2004	TGCGTGCAGCTCTGGGCCCCCAACCTCATCCAGCCCTCAACATCCCACCCGGGCCCTTACA	2063
Qy	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2064	GCTCCATGCAAGCTGCTGGAGACACAGAGTACAGTGCCTGCCAAGCTCTTGCAAGA	2123
Qy	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrc	702
Db	2124	TCTCCAGCCCTTGCTTGAAGACAGACAGTGGAGCCTGTGTCTCCAGACAGCTGCCCTTACT	2183
Qy	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2184	GTCCCGGGCGGGCAGGGGAGTGGAGCTCCGCCACCGTGAAATGCCTTGACTCTCAGACA	2243
Qy	722	erGluAlaValTyrgluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis	742
Db	2244	GCAGGCAGTTTATAGATTACACAGAGATGCCCAGACACAGCACTCCGGGACCCCCACA	2303
Qy	742	erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2304	GC--CGGCGCAACGGAGCTGGGCCAGATGCAGAGCCCCAGCTCTGTGCTGGCCTTCT	2360
Qy	762	rpArgLeuIleCysAspThrPheArgLysIleValaAspSerLysTyrsPheGlyArgGlyI	782
Db	2361	GGAGGCTTAATCTGTGACACCTTCCGAAAGATTGTGGACAGCAAGTAGTCTTTGGCGGGGAA	2420
Qy	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrrHisGluGlnProG	802
Db	2421	TCAATGATCGGCATCTCTGTGTCACACACTCAGCATGGGCATTCGAATATCCAGCAGCGCCG	2480
Qy	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2481	AGAGCTTACCAAGCCCTAGAAATCAGCAACATCGTCTTTCACAGGCTCTTTGGCCTGG	2540
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RESULT 10

AF190860

LOCUS

DEFINITION

 7349 bp mRNA linear
 Homo sapiens low voltage-activated T-type calcium channel alpha 1G

PRI 23-FEB-2000

splice variant CavT.1a (CACNA1G) mRNA, complete cds.

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VERSION     AF190860.1
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REFERENCE   1 (bases 1 to 7349)
            Cribbs, L.L., Gomora, J.C., Daud, A.N., Lee, J.H. and Perez-Reyes, E.
            Molecular cloning and functional expression of Ca(v)3.1c, a T-type
            calcium channel from human brain
            FEBS Lett. 466 (1), 54-58 (2000)
MEDLINE     20115462
PUBMED      10648811
REFERENCE   2 (bases 1 to 7349)
            Cribbs, L.L., Gomora, J.C., Lee, J.-H., Daud, A.N. and Perez-Reyes, E.
            Direct Substitution
            Submitted (29-SEP-1999) Physiology, Loyola University Medical
            Center, 2160 South First Avenue, Maywood, IL 60153, USA
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ORIGIN
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Query Match: 92.18% Indels: 8
DB: 9 Gaps: 4
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AUTHORS Dubin,A.B., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.			
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 7253)
 AUTHORS Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and
 Nargeot,J.
 TITLE Molecular and functional properties of the human alpha (1G) subunit
 that forms T-type calcium channels
 J. Biol. Chem. 275 (9), 6090-6100 (2000)
 MEDLINE 20158909
 PUBMED 10692398
 REFERENCE 2 (bases 1 to 7253)
 Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
 Direct Submission
 TITLE Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.
 JOURNAL 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN

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Qy 582 laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA 602
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Qy 602 laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT 622
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Qy 622 yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV 642
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Qy 642 alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS 662
Db 2004 TGGCTGCCAGTCTGGGCCCCACCTTACACAGGCTCAACATCCACCCGGGCTTAC 2063
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Qy 702 ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspS 722
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Qy 762 rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
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Qy	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
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Db	2841	GCAAGTTTGCTCTTGAGCGGATGGGACACCCCTGCCAGACCGGAAGAAATTTTGACTCCT	2900
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Qy	1002	laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValaspG	1022
Db	3081	CGGAGGGAGATGCCAACAGTCCGAATCAGAGCCGCAATTTCTTCTCACCCAGCGCTGGATG	3140
Qy	1022	lyAspGlyAspArgLysIleValAlaLeuValAlaLeuGlyGluHisAlaGluLeuA	1042
Db	3141	GTGATGGGGACAGAGAAGTGTGTGGCTTGGTGTCCCTGGGAGAGCATCCCGAGGCTGC	3200
Qy	1042	rgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL	1062
Db	3201	GGAGAGCCTGCTGTCGCGCTCTCATCATCCACAGCGCGCCACACCATGTGCTGCCTGCCA	3260
Qy	1062	ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerS	1082
Db	3261	AGAGCACAGCACGGGCTGGCGAGCGCTGGCGCTGGCGCTGGCGCGCAGCAGCAGCA	3320
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Qy	1102	erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA	1122
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Qy	1202	erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT	1222
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Qy	1222	hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuS	1242
Db	3738	CCCTGGCGCCTGATGACCCCCCACTGATGGGGATGACGGCGATGACAGGGGCACACTGA	3797
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 DEFINITION Sequence 3 from patent US 6358706.
 ACCESSION AR201014
 VERSION AR201014.1 GI:20251902
 KEYWORDS Unknown.

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 6822)
 AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
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 JOURNAL Patent: US 6358706-A 3 19-MAR-2002;
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 Query Match: 91.03% Indels: 31
 DB: 6 Gaps: 5

US-09-611-257A-24 (1-2287) x AR201014 (1-6822)

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QY	54	SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp	73
Db	62	GGCTCAACGACCTGTCTGGGGGGCGGGGGCGGGGGCGGGGTTCAGACGAAAGGACC	121
QY	73	roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValp	93
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QY	93	hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	113
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REFERENCE 1 (bases 1 to 6822)
AUTHORS Montell,A., Chemin,J., Bourinnet,E., Mennessier,G., Lory,P. and
Nargeot,J.
Molecular and functional properties of the human alpha (1G) subunit
that forms T-type calcium channels
J. Biol. Chem. 275 (9), 6090-6100 (2000)
JOURNAL MEDLINE
PUBMED 10692398
REFERENCE 2 (bases 1 to 6822)
AUTHORS Montell,A., Mennessier,G., Bourinnet,E., Lory,P. and Nargeot,J.
Direct Submission
TITLE Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
JOURNAL U.P.R. 1142, 141 rue de la Cardonville, Montpellier 34396, France
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393 yrPheValMetAspAlaHisSerPheTyTrpAsnPheIleTyTrpPheIleLeuLeuIleV 413
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DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1G subunit		
ACCESSION	AF227746		
VERSION	AF227746.1	GI:7159264	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 6897)		
AUTHORS	Monteil, A., Chemin, J., Bourin, E., Mennessier, G., Lory, P., and Nargeot, J.		
TITLE	Molecular and functional properties of the human alpha (1G) subunit that forms T-type calcium channels		
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
MEDLINE	20158909		
PUBMED	10692398		
REFERENCE	2 (bases 1 to 6897)		
AUTHORS	Monteil, A., Mennessier, G., Bourin, E., Lory, P., and Nargeot, J.		
TITLE	Direct Submission		
JOURNAL	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France		
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ORIGIN

Alignment Scores:

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 Score: 10936.00
 Length: 6897
 Matches: 2111
 Percent Similarity: 93.01%
 Conservative: 32
 Best Local Similarity: 91.62%
 Mismatches: 105
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 Indels: 56
 DB: 9 Gaps: 5

US-09-611-257A-24 (1-2287) x AF227746 (1-6897)

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QY	54	SerSerThrThrCysProGlyAla-AlaGlyAla-GlySerThrGluLysAsp	73
Db	62	GGCTCAACGACCTGTCGGGGCGCGGGCGCGGGCGGGGTCAGCAGAAAAGGACC	121
QY	73	roGlySerAlaAspSerGluAlaGluGlyLeuProTyProAlaLeuAlaProValValP	93
Db	122	CGGGCAGCGCGACTCCGAGCGAGGGGCTGCCGTACCCGCGCTGGCCCGGTGT	181
QY	93	hePheTyLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsp	113
Db	182	TCTTCTACTTGAGCCAGACAGCCCGCGGAGTGTGTCTCCGACGGTCTGTAAAC	241
QY	113	roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP	133
Db	242	CCTGGTGGAGCGCATGAGCATGTTGGTTCATCTTCTCACTCGCTGACCCCTGGCATGT	301
QY	133	heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA	153
Db	302	TCCGGCCATGCGAGACATCGCTGTGATCTCCACGCTCGCGGATCTTGCAGGCTTTG	361
QY	153	spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI	173
Db	362	ATGACTTCATCTTGGCTTCTTTCCTGCGGAGATGTTGTTGAAGATGTTGGCTTGGCA	421
QY	173	lePheGlyLysLysCysTyrLeuGlyAspThrTyrPheAsnArgLeuAspPheIleValI	193
Db	422	TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAACCGGCTTGACATCTTCATCGTCA	481
QY	193	leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
Db	482	TGCGAGGATGCTGAGTACTCGCTGGACCTGCAACAGCTCAGCTTCTCAGCTGCAGGA	541
QY	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
Db	542	CAGTCCGTGTCGCGACCGCTCAGGGCCATTAACCGGGTCCCAAGCATGCGCATCTTG	601
QY	233	alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV	253
Db	602	TCACTGCTGCTGATGCTGCTGCCCATGCTGGGCAACGCTCTCTGCTGCTCTCTCTCG	661
QY	253	alPhePheIlePheGlyIleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCTTCTTCTATCTTGGCATCGTGGCGCTCCAGCTGTGGGAGGGCTGCTTTCGGAACCG	721

QY 273 ySPheLeuProGluAAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
DB 722 GCTTCCTACCTGAGAAATTTTCAGGCTCCCTCGAGGTGGACCTGGAGCGCTATTACCA 781
QY 293 hrGluAAsnGluAAspGluSerProPheileCysSerGlnProArgGluAAsnGlyMetArgS 313
DB 782 CAGAGAAACGAGGATGAGAGCCCTTCATCTGCTCCACAGCCACGCGAGAACGGATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
DB 842 CTTGCAGAACGGTGCCTGCGCGGGAGCGGGGGCGGTGGCCACCTTGGCGTCTGG 901
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DB 902 ACTATGAGGCTCAACACAGCTCCAGCAACACCACTCTGTCTCACTGGAACCACTACTACA 961
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DB 962 CCAACTGCTCAGCGGGGGAGCAACACCTTCAAGGGCGCATCAACTTTGACAACATTG 1021
QY 373 lYTrAlaTrpIleAlailePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
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DB 1082 ACTTTGTGATGATGCTCATCTTCTTACAAATTTCACTTCACTTCTCTCATCATCG 1141
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Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFIO_spool/US09611257/runat_26042005_150448_14882/app.query.fasta_1.2439
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257_QCGN_1.1_963 @runat_26042005_150448_14882 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq 16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2002as.*

6: Geneseqn2002bs.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2003ds.*

11: Geneseqn2004as.*

12: Geneseqn2004bs.*

13: Geneseqn2004ds.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12024	100.0	7540	5 AAF31677	Aaf31677 Rat alpha
2	11980	99.6	6942	13 ADS16295	Ads16295 Rat volca
3	11829	98.3	7286	3 AAZ52309	Aaz52309 Rat pancr
4	11798	98.1	6762	2 AAX83485	Aax83485 Rat T-typ
5	11767	97.8	6816	2 AAX83487	Aax83487 Rat T-typ

6	11751.5	97.7	6795	2	AAX83486	Aax83486 Rat T-typ
7	11747.5	97.7	6741	4	AAX83488	Aax83488 Rat T-typ
8	11066.5	92.0	7741	4	AAD04756	Aad04756 Human T-t
9	10970	91.2	6750	2	AAX83481	Aax83481 Human T-t
10	10946	91.0	6804	2	AAX83483	Aax83483 Human T-t
11	10923.5	90.8	6783	2	AAX83482	Aax83482 Human T-t
12	10919.5	90.8	6729	2	AAX83484	Aax83484 Human T-t
13	10916	90.8	6892	5	AAF31684	Aaf31684 Human alp
14	10845.5	90.2	7648	13	ADQ89063	Adq89063 Human uro
15	10845.5	90.2	7648	13	ADS16298	Ads16298 Human vol
16	10843.5	90.2	8002	4	AAH98402	Aah98402 Human EST
17	6248	51.9	8447	5	AAF31678	Aaf31678 Rat alpha
18	6243	51.9	7898	2	AAF59081	Aaf59081 Human act
19	6242	51.9	7898	8	ABZ58365	Abz58365 Human T-t
20	6241	51.9	7898	2	AAX59080	Aax59080 Human act
21	6103	50.7	3993	4	AAS01624	Aas01624 Human T-t
22	5895	49.0	6132	2	AAX83489	Aax83489 Human T-t
23	5886	48.9	6114	2	AAX83490	Aax83490 Human T-t
24	5738.5	47.7	6941	2	AAX59082	Aax59082 Human act
25	5432.5	45.2	6990	13	ADS16296	Ads16296 Human vol
26	5420	45.1	6816	6	AAS16826	Aas16826 Human T-t
27	5420	45.1	6816	8	ABX93560	Abx93560 Human CDN
28	5420	45.1	6816	12	ADH69264	Adh69264 Human TCC
29	5420	45.1	6855	6	AAS16827	Aas16827 Human T-t
30	5420	45.1	6855	8	ABX93561	Abx93561 Human CDN
31	5420	45.1	6855	12	ADH69266	Adh69266 Human TCC
32	5407	45.0	6503	12	ADH69275	Adh69275 Rat TCCV
33	5346.5	44.5	5469	2	AAX83491	Aax83491 Human T-t
34	5345	44.4	5505	2	AAX83492	Aax83492 Rat T-typ
35	5200.5	43.2	5735	5	AAF31679	Aaf31679 Rat brain
36	3950	32.8	5562	2	AAV57542	Aav57542 Human cal
37	3950	32.8	5562	5	AAF31674	Aaf31674 Human cal
38	3937.5	32.7	7969	4	ABL07263	Ab107263 Drosophil
39	3861.5	32.1	6073	13	ADS16299	Ads16299 C. elegans
40	3399.5	28.3	6933	5	AAS75141	Aas75141 DNA encod
41	3356	27.9	2212	5	AAF31681	Aaf31681 Human alp
42	2091.5	17.4	3464	4	AAK94358	Aak94358 Human ful
43	2091.5	17.4	3464	12	ADL31040	Adl31040 Full leng
44	1974	16.4	1669	2	AAX59083	Aax59083 Human act
45	1751.5	14.6	7362	2	AAQ37817	Aaq37817 Sequence

ALIGNMENTS

RESULT 1
AAF31677
ID AAF31677 standard; cDNA; 7540 BP.

AC AAF31677;

DT 09-APR-2001 (first entry)

DE Rat alpha-IG calcium channel cDNA.

XX Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;
XX Rat; hypotensive; cardiant; nootropic; T-type calcium channel subunit;
XX Rat; cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;
XX Rat; epilepsy; alpha-IG calcium channel; ss.
XX Rattus sp.
XX WO200102561-A2.
XX 11-JAN-2001.

PF 04-JUL-2000; 2000WO-CA000794.

PR 02-JUL-1999; 99US-00346794.

XX (NEUR-) NEUROMED TECHNOLOGIES INC.

PI Snutch TP, Baillie DL;

XX

DR WPI; 2001-123111/13.
 DR P-PSDB; AAB66475.
 XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
 PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
 PT epilepsy.
 XX
 PS Example 2; Page 61-63; 103pp; English.
 XX
 CC The present sequence is given in a specification providing sequences and
 CC partial sequences for three types of mammalian (human and rat) T-type
 CC calcium channel subunits. An expression cassette has been generated which
 CC comprises a nucleotide sequence encoding a T-type calcium channel alpha₁
 CC subunit operably linked to control sequences to effect its expression.
 CC The novel calcium channel nucleic acids and proteins are useful for
 CC treating conditions characterised by undesirable levels of T-type calcium
 CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
 CC hypertension, sleep disorder and epilepsy
 XX
 SQ Sequence 7540 BP; 1502 A; 2313 C; 2161 G; 1564 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 7540
 Score: 12024.00 Matches: 2286
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.97% Indels: 0
 DB: 5 Gaps: 0

US-09-611-257A-24 (1-2287) x AAF31677 (1-7540)

QY	1	MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg	20
DB	385	ATGCTCCCCACCGGGTCCCGCTGGTGGAGACACCTCTCTGAGGGCTCCGCTCGC	444
QY	21	ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu	40
DB	445	CCCTCTTCGAGACCCCGGGGCCCCGCTGGCCAGAGATGGACGAGGAGGATGGAG	504
QY	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGly	60
DB	505	CGGGCGCGAGGAGTGGGACAGCCCGTAGCTTACCGCAGCTCAACGACCTGCGGGG	564
QY	61	ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla	80
DB	565	CCGGGGCGCGAGGGCGGGTCCGACGAAAGACCCGGGCGAGCGCGAGCTCCGAGCGC	624
QY	81	GluGlyLeuProTrpProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSer	100
DB	625	GAGGGGCTGCGTACCCCGGCTAGCCCGGTGGTTCCTTCTTACCTTGACCCAGGACAGC	684
QY	101	ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet	120
DB	685	CGCCCGCGAGCTGCTCTCCGACCGTCTGAACCGTGTTCGAGCGAGTCAGTATG	744
QY	121	LeuValIleLeuLeuAnCysValThrLeuGlyMetPheArgProCysGluAspIleAla	140
DB	745	CTGTGCTATCTTCTCACTGTGTGACTCTGGTATGTTTACGGCGGTGAGGACATTGCC	804
QY	141	CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePhe	160
DB	805	TGTGACTTCCACGCTGCCGATCTCTGAGGCTTCGATGACTTCATCTTTGCTCTTT	864
QY	161	AlaValGluMetValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeu	180
DB	865	GCTGTGAAATGGTGTGAAGATGGTGGCTTGGGCTCTTTGGGAAAGAAATGTATCTG	924
QY	181	GlyAspThrTrpAnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSer	200
DB	925	GGAGACACTTGGAAACCGCTTGACTTTTTCATTGTCATTCAGGAGATCTGGAGTATCG	984
QY	201	LeuAspLeuGlnAnValSerPheSerAlaValArgThrValArgValLeuArgProLeu	220

DB	985	CTGACCTGCAGAACGTTCAGCTTCTCCGACGTACAGGACAGTCCGTGTGTCGACCGCTC	1044
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu	240
DB	1045	AGGGCCATTAAACCGGGTCCCGAGCATTCGTTCATCTACTCTGTCGACACCTTG	1104
QY	241	ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal	260
DB	1105	CCTATGCTGGGCAACGTCTCTGCTCTGTTTCTTCGCTCTTTTCATCTTTGGCATCGT	1164
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
DB	1165	GGGTCACAGCTGGGGCAGGACTGCTTCGCAACCGTCTCTCTCCCGAGAACTTCAGC	1224
QY	281	LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro	300
DB	1225	CTCCCGCTGAGCGTGAGCTTGAGCGCTTATTACACAGACAGAAATGAGACGAGAGCCC	1284
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
DB	1285	TTCACTCTGCTCTACGCTTCGGGAGATGGCATGAGATCTCGCAGGAGTGTGCCACACTG	1344
QY	321	ArgGlyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer	340
DB	1345	CGTGGGGAAGCGGTGGTGGCCACCTCGAGCTATGGACTATGAGACCTATAACAGTTCC	1404
QY	341	SerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis	360
DB	1405	AGCAACACACCTGTGTCACTGGAAACAGTACTATACCACTGCTCTGCGGGCGAGCAC	1464
QY	361	AsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePhe	380
DB	1465	AACCCCTTCAAGCGCCATCAACTTGCACAACTTGGCTATGCTGGATGCCATCTTC	1524
QY	381	GlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSer	400
DB	1525	CAGGTTCATCACACTGGAGGGCTGGGTGCGACATCATGTACTTCTGTAATGACCTCACC	1584
QY	401	PheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsn	420
DB	1585	TTCTACAACTTCATCTACTTCACTTCTCATCATCTGTTGGGCTCTCTTCTCATGATCAAC	1644
QY	421	LeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu	440
DB	1645	CTGTGCTGTTGGTGATTCGCCAGCATTTCTCCGAGACCAACAGCGGAGAGTCAGCTG	1704
QY	441	MetArgGluGlnArgValArgPheIleuSerAsnAlaSerThrLeuAlaSerPheSerGlu	460
DB	1705	ATGCGGGAGCAGCGGTGTACGATTTCTCTGTCCTCAATGTAGCACCTGGCAAGCTTCTCTGAG	1764
QY	461	ProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgIysAlaAla	480
DB	1765	CCAGGAGCTGTGTATGAGGAGCTACTCAAGTACCTGTTGTACATCTCCGAAAGCAGCC	1824
QY	481	ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerPro	500
DB	1825	CGAAGCTGCGCCAGGCTCTTAGGGCTATAGGGCTGCGGGCTGGGTCTCAGCAGCCCA	1884
QY	501	ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg	520
DB	1885	GTGGCCGTGTAGGGGAGGAGGCCCCAGCCAGTGGCGAGTGCATCGCTCACACCGCTGT	1944
QY	521	LeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHis	540
DB	1945	CTGTCTGTCCACACCTGTGTCCACACCATCACCCACCATCACCATCACCATCACCAT	2004
QY	541	AsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly	560
DB	2005	AATGGGACGCTCAGAGTTCCCGGGGCGAGCCAGAGATCCAGGACAGGAGTGCATATGGG	2064
QY	561	SerArgArgLeuMetLeuProProSerThrProThrProSerGlyGlyProProArg	580
DB	2065	TCTCGCGGGCTCATGTACACACCATCTTACACCCACTCTTCTCTGCGGGCCCTCCGAGG	2124

QY 581 GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCys 600
DB 2125 GGTGGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGGAGCCAGTCCGTTGC 2184
QY 601 GluAlaProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys 620
DB 2185 CAGGACCCCTCCAGATGCCATGCCATCGAGGCATCTGGTAGGACTGTGGGTAGTGGGAAG 2244
QY 621 ValTyrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuVal 640
DB 2245 GTGTACCCCACTGTGCATACAGCCCTCCACAGAGATCTGAAGGATAAAGCACTAGTG 2304
QY 641 GluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyPro 660
DB 2305 GAGGTGGCCCCAGCCCTGGGCCCCCAACCTCACAGCTTCAACATCCCACTGGGCC 2364
QY 661 PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys 680
DB 2365 TTCAGCTCCCATGACAAAGCTCTCGGAGACACAGATACGGGAGCTGCCATAGCTCTGC 2424
QY 681 LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
DB 2425 AAATCTCCAGCCCTTGCTCCAGGACAGACAGTGGAGCCCTGGCGGCGGACAGTTGTCC 2484
QY 701 TyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSer 720
DB 2485 TACTGTGCCGACAGGACAGGACGACAGTCCGCTGACCATGTCTGCTGACTCA 2544
QY 721 AspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro 740
DB 2545 GACAGCGAGGCTGTGTATGAGTTTACACAGAGCGCTCAGCACAGTGAACCTCCGGATCCC 2604
QY 741 HisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla 760
DB 2605 CACAGCGCGGCGACAGCGAGCCCTGGGCCAGATGACAGAGCTAGTTCTGTGTGGCT 2664
QY 761 PheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArg 780
DB 2665 TTCTGGAGGCTGATCTGTGACACATCCGGAAGATCGTAGTAGCAATATCTTTGGCCGG 2724
QY 781 GlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGln 800
DB 2725 GGAATCATGATCGCATCTCTGGTCAATACATCAGCATGGGCATCGAGTACCACAGCAG 2784
QY 801 ProGluLeuLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAla 820
DB 2785 CCCGAGAGGCTCACCAACGCCCTGGAAATCAGCAACATCGTCTCACAGCCCTTTGGCC 2844
QY 821 LeuGluMetLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyr 840
DB 2845 TTGGAGATGCTGTGAACCTGCTTGCTACGGTCCCTTTGGCTACATTAAAGATCCCTAC 2904
QY 841 AsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGly 860
DB 2905 AACATCTTTCATGTGTCATTGGTTCATCAGTGTGGGAGATTTGGGCCAGCAGGGA 2964
QY 861 GlyIleLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe 880
DB 2965 GGTGGCCCTGTGCGTGTGGGAGCTTCCCGCTGATGCGGGTGTGAAGCTGTGGCGCTTC 3024
QY 881 LeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThr 900
DB 3025 CTGCCGCCCTTGAGCGCCAGCTCGTGGTCTCATGAGACCATGAGCAACAGTGGCCACC 3084
QY 901 PheCysMetLeuLeuMetLeuPheIlePhePheSerIleLeuGlyMetHisLeuPhe 920
DB 3085 TTCTGCATGCTCTCATGCTGTTTCATCTTCACTTTCAGCATCTGGGCATGCATCTCTTT 3144
QY 921 GlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsp 940
DB 3145 GGTTCGAAGTTGCGATCTGAACGGGATGGGGACACGCTTGGCAGACCGGAAGAAATTCGAC 3204

QY 941 SerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLys 960
DB 3205 TCCTCTGCTCTGGGCCATCGTCACTGTCTTTAGATTTGACTCAGGAGACTGGAATAAA 3264
QY 961 ValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeu 980
DB 3265 GTCTCTCAACAACGGCATGGCTCCACATCGTCTTGGGCTGCTCTTTACTTTTCATCGCCCTC 3324
QY 981 MetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPhe 1000
DB 3325 ATGACTTTTGGCAACTATGTGCTTTAACTCTGCTGGGCCATTTCTTGTGGAAGGATTC 3384
QY 1001 GlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal 1020
DB 3385 CAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTCCGCCAGTGTG 3444
QY 1021 AspGlyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu 1040
DB 3445 GATGTGTATGGGGACAGAAAGAGCGCTTGGCCCTTGGGCTTTGGGAGAACACGCGAA 3504
QY 1041 LeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHis 1060
DB 3505 CTAGAAAGAGCCCTTTTGGCACCCCTCATCATACGCTCGCACACCAATGTCCAC 3564
QY 1061 ProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSer 1080
DB 3565 CCCAAGAGCTCCAGCACAGAGTGTGGGGAGCACTGGGCTCTGGCTCTCGACGTACCAGT 3624
QY 1081 SerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSerAla 1100
DB 3625 AGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAATGTTCGCCCAAGTGCC 3684
QY 1101 ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSer 1120
DB 3685 CGCAGTCCCCCGCACAGTCTCTGGAGTCGGCAAGCAGCTGGACACAGCGGCTCCAGC 3744
QY 1121 ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArg 1140
DB 3745 AGGAACAGCTGGGCCGGCCCCCAGCCCTAAACGGGAGGAGCCCGAGCGGAGCGAGG 3804
QY 1141 SerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSerSerGluGluAsp 1160
DB 3805 TCCTCTGCTGTGGAGAGGCGCAGGAGAGTCAAGATGAGGAGAAAGTTTCAGAGAGGAC 3864
QY 1161 ArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLys 1180
DB 3865 CGGCCAGCCCCAGCAGCAGTACCATGCCACAGGGGTTCTTTGGAACGTGAGGCCAAG 3924
QY 1181 SerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGly 1200
DB 3925 AGTTCTTTTGACCTGCTGCACACTCTGCAGGTGCGGGCTGCACCGCACAGCGCGGC 3984
QY 1201 ArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla 1220
DB 3985 CGAGACTCTGCTCTGAGCACCAAGACTGTAAATGGCAAGTCTGGCTTCAGGCGGTTTGGCC 4044
QY 1221 ArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyAsn 1240
DB 4045 CGCACCTCAGGAGCTGATCACCCCCCACTGGATGGGAGTATGACAAATGATGAGGAAAT 4104
QY 1241 LeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysArg 1260
DB 4105 CTGAGCAAGGGGAACGCATACAGCCTGGGTGAGATCCCGGCTTCTGCTGTGTCGA 4164
QY 1261 GluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeuCys 1280
DB 4165 GAGCAGATTCCTGTGTCGGCTATATCTTTCTCTCCTCAGTCAAGGTTTCTCTCTGTGT 4224
QY 1281 HisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsn 1300
DB 4225 CACCGGATCATCACCCACCAAGATGTTTGACCATGTGGTCTCTGTCATCATCTTCTCAAC 4284
QY 1301 CysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePhe 1320

Db	4285	TGTATCACCATCGCTATGTGAGCGCCCAAAATTGACAGCGCTGAGCGCATCTTC	4344	Db	5365	AAACTTGTGGCCTTTGGCTTCGCGCGTTTCTTCCAGGACAGGTGGAACACAGCTGGACCTG	5424
Qy	1321	LeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValIysVal	1340	Qy	1681	AlaIleValLeuLeuSerIleMetGlyIleThrIleuGluIleGluValAsnLeuSer	1700
Db	4345	CTGACCCCTCTCAACTACATCTTCACGGCAGTCTTTCTAGCTGAAATGACAGTGAAGTG	4404	Db	5425	GCTATTGTGTTCTGTGCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTGCG	5484
Qy	1341	ValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeu	1360	Qy	1701	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1720
Db	4405	GTGGCACTGGCTGGTGTCTTGGGAGCAGGCTACCTGCGCAGCAGCTGGAAATGTGCTG	4464	Db	5485	CTGCCCATCAACCCACCATCATCCGATATCATGAGGGTGTCTCCGCATTTGCTCGAGTTCTG	5544
Qy	1361	AspGlyLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSer	1380	Qy	1721	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeu	1740
Db	4465	GACGGCTGTGCTGCTCATCTCCGTCATCGATCGACATCTGCTGCTCCATGGTCTCCGACAGC	4524	Db	5545	AAGCTGTTGAAGATGGCTGTGGGCATGCGGCACCTGTGTCACACGGTGTGATGACGCGCTG	5604
Qy	1381	GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeu	1400	Qy	1741	ProGlnValGlyAsnLeuGlyLeuPheMetLeuPheIlePheAlaAlaLeu	1760
Db	4525	GGCACCAAGATCTTGGCATGTGAGGGTGTGGGCTGCTGGGACCTGCTGGTCCACTC	4584	Db	5605	CCCAGGTGGGGAACCTGGGACTTCTCTTCAATGTTATTTGTTTTCATCTTTTGAGACTCTG	5664
Qy	1401	ArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrIleuMetSerSerLeu	1420	Qy	1761	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1780
Db	4585	AGGTCATCAGCCGCGCCAGGACTGAAAGCTGGTGGTAGAGACTCTGATGTATCCCTC	4644	Db	5665	GCGGTGGAGCTCTTTGGAGACTTGGAGTGTGATGAGACACACCTTTGTGAGGGCTTGGGT	5724
Qy	1421	LysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeu	1440	Qy	1781	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1800
Db	4645	AAACCCATTGGCAACATTGGTGCATTTGCTGTGCCCTTCTTATCATTTTGTGAATCTC	4704	Db	5725	CGGCATGCCACCTTTAGGAACCTTTGGTATGGCCTTTCTGACCCCTCTCCGAGTCTCCACT	5784
Qy	1441	GlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyAspThrArgAsnIle	1460	Qy	1801	GlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThr	1820
Db	4705	GGGGTGCAGCTCTTCAAGAGGAAGTTCTTCGTGTGTGTCAGGGTGAGACACAGGAACATC	4764	Db	5785	GGTGCAACTGGAATGGTATTATGAGGACCTTCCCGGACTGTGACAGGAGTCCACC	5844
Qy	1461	ThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPhe	1480	Qy	1821	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1840
Db	4765	ACTAACAAATCCGACTGCGCTGAGGCAGCTACCGATGGTCCGGCACAAAGTACAACTTT	4824	Db	5845	TGCTACAAACACTGTCTCTCCCTATCTACTTGTGTCTTCTGCTGCTGACGCCCTCAGTTT	5904
Qy	1481	AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal	1500	Qy	1841	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1860
Db	4825	GACAACTGGCCGAGGCTCTGATGTCCCTGTTGTGCTGGCTTCCAGGATGGTGGGT	4884	Db	5905	GTGCTGGTCAACGTGGTCTATAGCTGTGTGTATGAGAACCTTGGAGAAAGAACACAAAG	5964
Qy	1501	AspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMetAsnHis	1520	Qy	1861	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerPro	1880
Db	4885	GACATCATGTATGATGGCTGGATGCTGTGGTGTGGATCAGCAGGCCCATCATGAACAC	4944	Db	5965	GCCAGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAGATGAGACGCTCAGCCG	6024
Qy	1521	AsnProTrpMetLeuTyrPheIleSerPheLeuLeuIleValAlaPheValLeu	1540	Qy	1881	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSer	1900
Db	4945	AACCCCTGGATGCTATATCT	5004	Db	6025	CAGCCCT	6084
Qy	1541	AsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGlu	1560	Qy	1901	ThrAsnSerProLysProGlyValAlaProHisThrAlaHisIleGlyAlaAlaSerGly	1920
Db	5005	AACATGTTTGTGGCGTGGTGGTGGAGAACTTCCATAAGTGCAGACAGCAGGAGGAG	5064	Db	6085	ACTGACAGCCCTTAGCCCTGGGCTCCACACACCACTGCCACATTTGGAGACGCTCGGGC	6144
Qy	1561	GluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgGlySer	1580	Qy	1921	PheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGly	1940
Db	5065	GAGGAGCGAGCGCGCTGAGGAGAGCAGTACGGAGGCTGGAGAAAGAGAGAGAGT	5124	Db	6145	TTCTCCCTTGGACACCCACGATGGTACCCACCCGAGGAGGTGCGAGTCCCTCTAGGA	6204
Qy	1581	LysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1600	Qy	1941	ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAsp	1960
Db	5125	AAGGAGAGCAGATGGCGGAGCCAGTGCAGGCCCTACTACTCTGACTACTCGAGATTC	5184	Db	6205	CCAGACCT	6264
Qy	1601	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1620	Qy	1961	SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGly	1980
Db	5185	CGGCTCTTGTCCACCACTGTGTACCAAGCCACTTACCTGGAGCTTCTCATCTCTGGTGC	5244	Db	6265	AGCTACATGTGCCCAATGGAGCACTGTGAGAGATCCCTAGGACACAGGCGCTGGGG	6324
Qy	1621	IleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1640	Qy	1981	LeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSer	2000
Db	5245	ATCGGGCTGAACGGTGGTCACTATGGCCATGGAACATTTACAGAGCCCGCAGATCTGGAC	5304	Db	6325	CTCCCAAAAGCCAGTCCAGCTCCATCTTGTCCGTCTACTCCCAACACAGACACACAGC	6384
Qy	1641	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPhe	1660	Qy	2001	CysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThr	2020
Db	5305	GAGGCTCTGAGATCTGCAATTTACATCTTTTACCGTCTCTTGTCTTTGAGTCAAGTTTC	5364	Db	6385	TGCTCTCTACAGCTTCCCAAGATGTGACTATCTCTCCAGCTCATGGGGCTCCACC	6444
Qy	1661	LysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1680	Qy	2021	TrpGlyValaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeu	2040
				Db	6445	TGGGGCGGCATCTCCATAAACTATCCCCACCTGGCGCTCCCTCTGCTGCTGAGGCGCTCTC	6504

QY 2041 ArgArgGlnAlaAlaileArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu 2060
 DB 6505 AGGCGCCAGGAGCAATAGAGTACTCTCGTGTGTGAGGGCTGGTAGCCGGGAA 6564
 QY 2061 AspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTyr 2080
 DB 6565 GACCTGTGTGACAGGTGAGTGGGCGCTCTGCGCTCTGACCGGTCTCATCTCTGG 6624
 QY 2081 GlyGlySerSerIleGlnValGlnGlnArgSerCysGlyLeuGlnSerIleValSerIleHis 2100
 DB 6625 GGGCGGTGAGCAATCCAGGTGACAGCGTTCGGCATCCAGAGCAAAAGTCTCCAAGCAC 6684
 QY 2101 IleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGlu 2120
 DB 6685 ATCGCTGTCAGCCCTTGGCCAGGCTGGAACCCAGCTGGGCAAGGACCTCCAGAG 6744
 QY 2121 ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuPro 2140
 DB 6745 ACCAGAGCAGCTTAGAGCTGGACACGAGCTGAGCTGGATTTCAGGAGACCTCTTCCC 6804
 QY 2141 SerSerGlnGluProLeuPheProArgAspLeuLysCysTyrSerValGluThr 2160
 DB 6805 AGCAGCCAGAGAACCCCTTTCACCGGACCTGAAGAAGTGTACAGTGTAGAGACC 6864
 QY 2161 GlnSerCysArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAla 2180
 DB 6865 CAGAGCTGAGGCGCAGCTGGTCTGGCTAGTAGAAGACGAGACACTCATTTGCT 6924
 QY 2181 ValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGly 2200
 DB 6925 GTGAGCTGTCTGGACAGCGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCGG 6984
 QY 2201 GlyGlnProLeuGlyProGlySerArgProLysLysLysLeuSerProSerIle 2220
 DB 6985 GGCCAACTCTTGGGGTCTCGGAGCGCGCTTAAGAAACCTCAAGCCACCCAGTATC 7044
 QY 2221 SerIleAspProProGluSerGlnGlySerArgProCysSerProGlyValCysLeu 2240
 DB 7045 TCTATAGACCCCGGAGAGCAGGCTCTCGGCCCCATGCACTCTGTGTCTGCTC 7104
 QY 2241 ArgArgAlaProAlaSerAspSerLysAspProSerValSerProLeuAspSer 2260
 DB 7105 AGGAGGAGGCGCGCGCAGTACTTAAGATCCCTCGGTCTCCAGCCCTTGACAGC 7164
 QY 2261 ThrAlaIleSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAsp 2280
 DB 7165 ACAGCTGCTCACCCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTTGTCTCTGAC 7224
 QY 2281 ProThrAspMetAspPro 2286
 DB 7225 CCAACAGACATGGACCCC 7242

RESULT 2
 ADS16295
 ID ADS16295 standard; DNA; 6942 BP.
 XX
 AC ADS16295;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.
 XX
 KW Voltage-dependent ion channel; drug candidate;
 KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
 KW anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.
 XX
 OS Rattus norvegicus.
 XX
 PN US2004175761-A1.
 XX
 PD 09-SEP-2004.
 XX

PF 01-MAR-2003; 2003US-00377139.
 PR
 XX 01-MAR-2003; 2003US-00377139.
 PA (MACK/) MACKINNON R.
 PA (MACK/) MACKINNON A L.
 PA (JIAN/) JIANG Y.
 PA (RUTA/) RUTA V.
 XX
 PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
 XX WPI; 2004-642122/62.
 DR REFSEQ; NM_031601.
 XX
 PT Screening drug candidates that target voltage dependent ion channel
 PT protein, involves contacting screening protein with chemical compound,
 PT which is drug candidate and determining whether chemical compound binds
 PT to screening protein.
 XX
 PS Disclosure; SEQ ID NO 7; 61pp; English.
 XX
 CC The invention relates to the composition of matter suitable for use in
 CC identifying chemical compounds that bind to voltage-dependent ion channel
 CC proteins. The composition comprises a screening protein that consists of
 CC an ion channel voltage sensor domain of the ion channel protein
 CC immobilised on a solid support. The invention is useful for identifying
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion
 CC channel proteins. The drug candidate of the invention is utilised for
 CC treating a condition mediated by aberrant electrical activity that
 CC initiates uptake or release of neurotransmitters and contraction of
 CC muscles. The drug candidate of the invention is also utilised for
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-
 CC dependent calcium channel DNA.
 XX
 SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 6942
 Score: 11980.00 Matches: 2283
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 3
 Query Match: 99.60% Indels: 2
 DB: 13 Gaps: 0
 US-09-611-257A-24 (1-2287) x ADS16295 (1-6942)
 QY 1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20
 DB 16 ATGCTCCCCCAGCGGTCTCCCGCTTGGTGAGGACACCTCTCTGAGGGGCTCCGCTCGC 75
 QY 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGlu 40
 DB 76 CCCTCTTCGAGACCCCGGGGCCCCCGCTGCGCAGAGATGGACGAGGAGATGGAG 135
 QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
 DB 136 CGGCGCGCGAGAGTGGGACACCCCGTAGCTTCAGCGAGCTCAACGACCTGCTCCGGG 195
 QY 61 ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGlu 80
 DB 196 CCGGGCGCGCGAGGGGCGGGGTCGACGGAAGAGACCCGGCGAGCTCCGAGG 255
 QY 80 laGluGlyLeuProTyrProAlaAlaProValValPhePheTyrLeuSerGlnAsp 100
 DB 256 CGAGGGGCTGCGGTATCCCGCGCTAGCCCGGTGGTTCCTTCTACTTGAGCCAGGACA 315
 QY 100 erArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerM 120
 DB 316 GCGCGCGCGAGCTGGTGTCTCCGACCGGTCTGTAAACCCGCTGGTTCGAGGAGTCA 375
 QY 120 etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA 140
 DB 376 TGCTGCTCATCTCTCAACTGTGTGACTCTGGGTATGTTTCAGGCCCGCTGTGAGGACATTG 435

140 laCysAspSerGlnArgCysArgGluLeuGlnAlaPheAspPheIlePheAlaPheP 160
 436 CTTGTGACTCCAGAGCGCTGCGGATCCTCGAGCCCTTCGATGACTTCATCTTTGCTTCT 495
 160 heAlaValGluMetValVallyMetValAlaLeuGlyIlePheGlyIlylsCysTyrL 180
 496 TTGCTGTGAAATGGTGTGAAGATGGTGGCTTGGGCATCTTTGGGAAGAATTTACC 555
 180 euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200
 556 TGGGAGACACTTGGAAACCGGCTGACTTTTTCATTTGTCTATCGACGGATGCTGGAGTAT 615
 200 erLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProL 220
 616 CGCTGGACCTGCAGAACGTCAGCTTCTCCGAGTCAGGACAGTCGCTGTGTCGACCGC 675
 220 euArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL 240
 676 TCAGGGCCATTAACCGGGTGCCAGCATGGCAATCTCGTCAATTTACTGTGGACACT 735
 240 euProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleV 260
 736 TGCCTATGTGGCAAGCTCTGCTGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCT 795
 260 alGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheS 280
 796 TGGCGTCCAGCTGTGGCAGGACTGCTTGGCAACCGGCTTCTTCTTCTTCTTCTTCTTCT 855
 280 erLeuProLeuSerValAspLeuGluProTyrTrpGlnThrGluAsnGluAspGluSerP 300
 856 GCCTTCCCTCCAGCGTGAGCTGGAGCTTATTTACAGACAGAGATGAGGACGAGGCC 915
 300 roPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrL 320
 916 CTTTCATCTCTCAGCTCGGGAGAAATGGCATGAGATCCTGCAGGAGTGTGCCACAC 975
 320 euArgGlyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS 340
 976 TGCCTGGGGAAGCGGTGGTGGCCACCTCGAGCTCGGACTATGAGACCTATTAACAGTT 1035
 340 erSerAsnThrThrCysValAsnTrpAsnGlnTyrTrpThrAsnCysSerAlaGlyGluH 360
 1036 CCAGCAACACCATGTTGTCACTGGAAACCACTATATCACTTCTTCTTCTTCTTCTTCTTCT 1095
 360 isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP 380
 1096 ACAACCCCTTCAAAGGGCCATCAACTTGCACACATTTGGCTATGCTTGGATCGCCATCT 1155
 380 heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisS 400
 1156 TCCAGGTTCATCACACTGAGGGCTGGGTGGACATCATGTACTTGTATGAGCGCTCACT 1215
 400 erPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleA 420
 1216 CTTTCTACAACTTCATCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1275
 420 snLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL 440
 1276 ACCTGTGCTGTGTGTATGCCAGCATGTTCTCCGAGACCAACACGCGGAGAGTCCAGC 1335
 440 euMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerG 460
 1336 TGATCGGGAGCAGCGTGTACGATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1395
 460 luProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgIlyAlaA 480
 1396 AGCCAGGCGAGCTGTATGAGGAGTACTCAAGTACTCTGGGTATCATCTCCGAAAGCAG 1455
 480 laArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP 500
 1456 CCCGAAGGCTGGCCCGAGGTCTCTAGGGCTATAGGGCTGGGGCTGGCTGTCCAGCAGCC 1515

500 roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA 520
 1516 CAGTGGCCCGTAGTGGCAGAGCCCGAGCCAGTGGCAGTGCACCTCGCTCACACCGTC 1575
 520 rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisLeuG 540
 1576 GTCTGTCTGTCCACCACCTGGTCCACCACCATCACACCACCATCACCATCACCATCTGG 1635
 540 lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG 560
 1636 GTATGGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGGACAGGATGCCAATG 1695
 560 lySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA 580
 1696 GGTCTTCCCGGCTCATGTACACCACTTACACCACTTCCCTCTGGGGGCTCCCGA 1755
 580 rgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgC 600
 1756 GGGGTGGGAGTCTGTATACAGCTTCTACCATGTGTACTGCCACTTGGAGCCAGTCCGTT 1815
 600 ysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
 1816 GCCAGGACACCCCTCCAGATGCCATCGGAGGCACTTGTGTAGACTGTGGGTAGTGGGA 1875
 620 ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV 640
 1876 AGGTGTACCCCACTGTGCATACCAAGCCCTCCACAGAGATACTGAAGGATAAAGCACTAG 1935
 640 alGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP 660
 1936 TGGAGTGGCCCGCCAGCCCTGGGCCCCCACCCTCACAGCTTCAACATCCACCATCTGGGC 1995
 660 roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC 680
 1996 CTTTCAGCTCCATGCACAGCTCCTTGGAGACACAGAGTACGGAGCCTGCCATAGTCTCT 2055
 680 ysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP 700
 2056 GCAAAATCTCCAGCCCTTGTCTCCAGGCGAGCAGTGGAGCCTTGGGGCCGAGCACTTGTCT 2115
 700 roTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspS 720
 2116 CTTACTGTGCCCGGACAGGACGAGGAGCAGAGTCCGCTGACCATGTCTATGCTGACT 2175
 720 erAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspP 740
 2176 CAGACAGCGAGCTGTGTATGAGTTACACAGACGCTCAGCACAGTACCTCCGGGATC 2235
 740 roHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA 760
 2236 CCCACAGCGCGGCGACAGCGAGCCTGGGCCAGATGCAGAGCTTAGTCTGTGCTGG 2295
 760 laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA 780
 2296 CTTTCTGGAGGCTGATCTGTGACACATTCGGAAGATCGTAGATAGCAAAATCTTTGGCC 2355
 780 rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800
 2356 GGGGAATCATGATCGCCATCTCTGGTCAATACACTCAGCATGGGCATCGAGTACCAGAC 2415
 800 lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820
 2416 AGCCCGAGGAGCTCACCAACCGCTGGAATCAGCAACATCGTCTTCCACGAGCTCTTCC 2475
 820 laLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProT 840
 2476 CTTTGGAGATGCTGTCTGAAACTCTTGTCTTACGGTCCCTTTGGCTACATTAAGAAATCCCT 2535
 840 yrAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnGlnG 860
 2536 ACAACATCTTTGATGGTGTCTTGTGTCTCATCTGTGTGGGAGATTTGGGGCCAGCAGG 2595
 860 lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP 880

Db	2596		GAGGTGGCTGTGGTGTGGGACCTTCCGCTGATGGGGTGTGAAGCTGGTGGCT	2655
Qy	880	heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT	900	
Db	2656	TCCTGGCGGCGCTGCAGCGCAGCTCGTGGTGTCTCATGAAGACCATGGAACGTGGCCA	2715	
Qy	900	hrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuP	920	
Db	2716	CTTCTGCATGCTCTCATGCTGTTCATCTTCATCTTCAGCATCTGGGCATGCATCTCT	2775	
Qy	920	heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA	940	
Db	2776	TTGGTTGCAAGTTCCGATCTGAACCGGATGGGACAGCTTGCCACAGCGGAATTTCCG	2835	
Qy	940	spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL	960	
Db	2836	ACTCCCTGGCTTGGGCCATCGTCACTGTCTTTCAGATTCAGACTCAGGAAGACTGGAA	2895	
Qy	960	ysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaL	980	
Db	2896	AAGTCTCTACACGGCATGGCTCCACATCGTCTTGGGCTGCTCTTTACTTTCATCGCC	2955	
Qy	980	euMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP	1000	
Db	2956	TCATGACTTTTGGCAACTATGTGCTCTTAACCTGTGCTGGTGGCCATCTTGTGGAAG	3015	
Qy	1000	heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV	1020	
Db	3016	TCCAGGCGAGAGGAGATGCCAACAGTCTGAGTCAGAGCCGTGATTTCTTTTCCGCC	3075	
Qy	1020	alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG	1040	
Db	3076	TGATGTGTATGGGACAGAAAGAGCGCTTGGCCCTTGGTGGCTTGGGAGAACACCGG	3135	
Qy	1040	luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH	1060	
Db	3136	AACCTACGAAAGAGCTTTTGGCACCCCTCATCTATCCATCCAGCTGCGACACCAATG	3195	
Qy	1060	isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrS	1080	
Db	3196	ACCCCAAGAGCTCCAGACAGGTGTGGGGAGACACTGGGCTCTGGCTCTCGACGTACC	3255	
Qy	1080	erSerSerGlySerAlaGluProGlyAlaHisHisGluMetLysCysProProSerA	1100	
Db	3256	GTAGCACTGGTTCGCTGAGCTGGAGCTGCCACCATGAGATGAATGTCCGCCAAGTG	3315	
Qy	1100	laArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerS	1120	
Db	3316	CCGCGAGCTCCCGCACAGTCCCTGGAGTGGCGCAAGCAGCTGGACCCAGCGGCTCCA	3375	
Qy	1120	erArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArgA	1140	
Db	3376	GCAGGAACAGCTGGGCGGCGGCCCCAGCCCTAAAGCGGAGGAGCCGAGCGGAGCGGA	3435	
Qy	1140	rgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluLysSerSerGluGluA	1160	
Db	3436	GGTCCCTGTCTGTGGAGAGGGCCAGAGAGTCAAGATGAGGAGAAAGTTTCAGAAAGG	3495	
Qy	1160	spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL	1180	
Db	3496	ACCGGGCCAGCCAGCAGGAGGTGACCATCGCCACAGGGGTTCCTTGGAAAGTGGAGCCA	3555	
Qy	1180	ysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG	1200	
Db	3556	AGAGTTCTTTGACTTCGCTGACACTCTGCAGGTGGCGGGCTGTCACCGCACAGCCAGCG	3615	
Qy	1200	lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA	1220	
Db	3616	GCCGGAGCTTCGCTCTGAGCACCAAGACTGTATGGCAAGTTCGGCTTCAGGGGCTTTGG	3675	
Qy	1220	laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGlyA	1240	

Db	3676	CCCGCACCTGTAGGACTGATGATGACCCCACTGGATGGGATGATGACAAATGATGAGGAA	3735	
Qy	1240	snLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA	1260	
Db	3736	ATCTGAGCAAAAGGGAAACGATACAGCCTGGGTGAGATCCCGCTTCTCGCTGTGGCC	3795	
Qy	1260	rgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuC	1280	
Db	3796	GAGAGCGAGATTCCTGGTGGCCTATATCTTCTCTCTCAGTCAAGGTTCGCTCCTGT	3855	
Qy	1280	ysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA	1300	
Db	3856	GTACCGGATCATCACCAAGATGTTGACCATGTGTGCTCTCGTCAATCATCTTCCTCA	3915	
Qy	1300	snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP	1320	
Db	3916	ACTGTATCACCATCGCTATGGAGCGCCCAAAATGACCCACAGCGCTGAGCGCATCT	3975	
Qy	1320	heLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysV	1340	
Db	3976	TCCTGACCCCTCTCCAACATCATCTTCACGGCAGTCTTTCTAGCTGAAATGACAGTGA	4035	
Qy	1340	alValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValL	1360	
Db	4036	TGGTGGCAGTGGCTGTGCTTTGGGAGCAGCGCTACCTGCGCAGCAGCTGGAATGTC	4095	
Qy	1360	euAspGlyLeuLeuValLeuSerValIleAspIleLeuValSerMetValSerAspS	1380	
Db	4096	TGACCGCTTGTGTGGTCTCATCTCCGTCACTGACATCTGGTCTTCATGGTCTCCGACA	4155	
Qy	1380	erGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProL	1400	
Db	4156	GCGCACCAAGATCCTTGGCATCTGAGGGTGTGCGGCTGCTGCGGACCTGCGTCCAC	4215	
Qy	1400	euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL	1420	
Db	4216	TCAGGGTTCATCAGCGCGGCGCAGGAGCTGAAGCTGGTGTGTAGAGACTCTGATGTG	4275	
Qy	1420	euLysProIleGlyAsnIleValIleValIleCysCysAlaPhePheIleIlePheGlyL	1440	
Db	4276	TCAACCCATTTGGCAACATTTGGTCAATTTGCTGTGCTTCTTCATCATTTTTTGGAA	4335	
Qy	1440	euGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnI	1460	
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Qy	1460	leThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTrpAsnP	1480	
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Db	4516	TTGACATCATGATATGAGCTGAGTGTGGTGTGGTGTGGATCAGCAGCCCATCATGA	4575	
Qy	1520	isAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValL	1540	
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Qy	1540	euAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluG	1560	
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Qy	1560	luGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgS	1580	
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Qy	1580	erLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgP	1600	
Db	4756	GTAAGGAGAGCAGATGGCCGAAAGCCAGTGCAGGCCCTACTACTCTCTCTCTCTCTCT	4815	

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 4816 TCGGGCTCTTGTCCACCACTGTGTACAGCCACTACCTGACCTCTTCACTGGTG 4875
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 1700 erLeuProIleAsnProThrIleIleArgIleMetArgValLeuAArgIleAlaArgValL 1720
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 1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgCysAspGlnGluSerT 1820
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 2240 euArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspS 2260
 6736 TCAGGAGGAGGCGCGCGCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCTTGTGACA 6795
 2260 erThrAlaAlaSerProSerProLysAspThrLeuSerLeuSerGlyLeuSerSerA 2280
 6796 GCACGGCTGCTCACCTCTCCCAAGAAAGACACGCTGAGTCTCTCTGTTGTCTCTCTG 6855
 2280 spProThrAspMetAspPro 2286
 6856 ACCCAACAGACATGGACCCC 6875

RESULT 3
 AAZ52309
 ID AAZ52309 standard; cDNA; 7286 BP.
 XX
 AC AAZ52309;

XX
DT
XX
DE
XX
XX
KW Rat; pancreatic T-type calcium channel alpha subunit; insulin;
KW pancreatic beta cell; alphaIG; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; L type calcium channel; NiDDM;
KW type II diabetes; non-insulin dependent diabetes mellitus; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT misc_feature 1..157
FT /tag= b
FT /note= "Region upstream to the coding region of
FT pancreatic T-type calcium channel protein"
FT CDS 2..7285
FT /tag= a
FT /product= "Pancreatic T-type calcium channel alpha
FT subunit"
FT /transl_except= (pos:11..13, aa:Xaa)
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FT /transl_except= (pos:7112..7114, aa:Xaa)
FT /note= "Xaa corresponds to in-frame stop codon. This
FT region includes sequence upstream to the coding region of
FT pancreatic T-type calcium channel protein. Does not
FT include stop codon"
FT /partial
FT mat_peptide 158..7285
FT /tag= c
FT /product= "Pancreatic T-type calcium channel alpha
FT subunit"
FT /note= "This region is claimed as SEQ ID NO: 1"
XX
PN WO200015845-A1.
XX
XX 23-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US019675.
XX
XX 26-AUG-1998; 98US-0098004P.
XX 27-JAN-1999; 99US-0117399P.
XX
XX (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
XX Li M;
XX
XX WPI; 2000-271475/23.
XX P-PSDB; AAY70720.
XX
XX Novel nucleic acids encoding pancreatic T-type calcium channels used for
XX regulation of T-type calcium channels and treatment of type II diabetes.
XX
XX Example 1; Page 114-119; 124pp; English.
XX
XX The present cDNA encodes a protein that includes pancreatic T-type
XX calcium channel alpha subunit derived from rat insulin secreting beta
XX cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-
XX type calcium channel alpha subunit (alphaIG). The T-type Ca2+ channel
XX from INS-1 (alphaIG-INS) and neuronal alphaIG are alternative splice
XX isoforms of the same gene. The INS-1 isoform is also expressed in brain,
XX neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+
XX channel belongs to the family of low voltage activated Ca2+ channels. The
XX present sequence is used for treating diseases associated with abnormal
XX expression or function of T-type calcium channels. They are especially
XX used for treating type II diabetes. Modulators of pancreatic T-type Ca2+
XX channel e.g. antisense oligonucleotides, ribozymes and inhibitors are
XX used in methods for modifying insulin secretion by pancreatic beta cells,
XX basal calcium levels, pancreatic L type calcium channel activity,
XX pancreatic cell death, pancreatic L type calcium channel proliferation and calcium
XX influx through L type calcium channels in cells

SQ Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 7286
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 3 Gaps: 2
US-09-611-257A-24 (1-2287) x AAZ52309 (1-7286)
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DB 58 ATGCTCCCAACCGGGTCCCCGGTTCGTGAGGACACCTCTCTGAGGGGCTCCGCTC 117
QY 20 rgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
DB 118 GCCTCTTTCGGACCCCGGGCCCGGGTGGCCAGAGATGACGAGGAGGATGG 177
QY 40 luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProG 60
DB 178 AGCGGGCGCGAGAGTTCGGGACAGCCCGGTAGCTTCACGAGCTCAACACCTGTCCG 237
QY 60 lyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGl 79
DB 238 GGCCTGGGGCCGCGAGGGCCGGGTTCGACGAAAGGACCCGGGCGAGGACTCCGA 297
QY 79 uAlaGluGlyLeuProTyProAlaLeuAlaProValValPhePheTyLeuSerGlnAs 99
DB 298 GCGGAGGGGCTGCCGTACCCCGGTAGCCCGGTGGTTCCTTCTACTTGAGCCAGGA 357
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119
DB 358 CAGCCGCCCGCGAGGTGGTGTCTCCGACGGTCTGTAAACCCGGTGGTTCGAGCGAGTCAG 417
QY 119 rMetLeuValLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIl 139
DB 418 TATGCTGGTCACTTCTCACTGTGTGACTCTGGGTATGTTTCAGGCCGTGTGAGGACAT 477
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPh 159
DB 478 TGCTCTGTGACTCCAGCGCTGCCGATCTCCGACGGCTTCGATGACTTCATCTTTGCTT 537
QY 159 ePheAlaValGluMetValVallyMetValAlaLeuGlyIlePheGlyIleCysTy 179
DB 538 CTTTGTCTGGAAATGGTGAAGATGGTGGCTTGGGCATCTTTGGGAAGAAATGTTA 597
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTy 199
DB 598 CTTGGGAGACACTTGGAAACGGCTTGACTTTTTCATTTGTCAGGGATGCTGGAGTA 657
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219
DB 658 TTCCTTGGACCTTCAGAACGTCAGCTTCCTCCGACGTCAGACAGTCCGTGTGTCGACC 717
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh 239
DB 718 GCTCAGGGCATTAACCGGGTGGCCAGCATTCCTCGTCACATTTACTGTCTGGACAC 777
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuLeuCysPhePheValPhePheIlePheGlyI 259
DB 778 CTTGCTATGTGGGCAACGTCCTGTGCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 837
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAenPh 279
DB 838 CGTGGCGCTCCAGCTGTGGGCGAGGACTGCTTCGCAACCGATGCTTCTCCCGAGAACTT 897
QY 279 eSerLeuProLeuSerValAspLeuGluProTyTrpGlnThrGluAsnGluAspGluSe 299
DB 898 CAGCTCCCGCTGAGCGTGAGCCCTTATTACAGACAGAGAAATGAGACGAGAG 957
QY 299 rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh 319

Db	958	CCCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGATCCTCAGGAGTGTGCCAC	1017	Db	2038	GCCCTTCAGCTCCATGCACAAGCTCTCGGAGACACAGAGTACGGGAGCCTGCCATAGCTC	2097
Qy	319	rLeuArgGlyGluGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSe	339	Qy	679	rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy	699
Db	1018	ACTGCGTGGGAAGCGGTGGTGGCCACCCCTGCGAGTCTGGAGTATGAGACTATAACAG	1077	Db	2098	CTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGAGCCTGCGGGCCGACAGTTG	2157
Qy	339	rSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyrThrAsnCysSerAlaGlyG1	359	Qy	699	sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs	719
Db	1078	TTCCAGCAACACCACCTGTGTACCTGGGAACAGTACTATACCAATCTCTCGCGGCGA	1137	Db	2158	TCCCTACTGTGCGCGGACAGAGCAGAGAGCCAGAGTCCGCTGACCATGTCTATGCTGA	2217
Qy	359	uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIleAlaI1	379	Qy	719	pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs	739
Db	1138	GCACAACCCCTTCAAGGGCGCCATCAACTTTCACAACATTTGGCTATGGCTGATCGCCAT	1197	Db	2218	CTCAGACAGCGAGGCTGTGTATGATTTTCAACAGGACCTCAGCACAGTACCTCCGGGA	2277
Qy	379	ePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHi	399	Qy	739	pProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValle	759
Db	1198	CTTCCAGGTGATCACACTGGAGGCTGGGTGGACATCATGTACTTCGTAAATGGACGCTCA	1257	Db	2278	TCCCCACAGCGCGCGGACAGCGGAGCCTGGGCGCCAGATGCAGAGCCTAGTTCTGTGCT	2337
Qy	399	sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetI1	419	Qy	759	uAlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG1	779
Db	1258	CTCCTTCTACAACCTCATCTACTTCTTCTTCATCATCTGCTGGGCTCTTCTTCATGAT	1317	Db	2338	GCTTTTCTGGAGGCTGATCTGTGACACATTCGCGAAGATCGTAGTAGCAATACTTTGG	2397
Qy	419	eAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG1	439	Qy	779	yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisG1	799
Db	1318	CAACCTGTGCTGCTGATTCGCCAGCGAGTTCTCCGAGACCAACACGCGGAGAGTCA	1377	Db	2398	CCGGGAATCATGATCGCCATCTCTGGTCAATACACTCAGCATGGGCATCGAGTACCACGA	2457
Qy	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459	Qy	819	uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh	839
Db	1378	GCTGATCGGGAGGAGCGGTGTACGATTCCTGTCCTCAATGTAGCACCTTGGCAAGCTTCTC	1437	Db	2458	GCAGCCCGAGGAGGCTCACCAACGCCCTGGAAATCAGCAACATCTCTTACCAGCCTCTT	2517
Qy	459	rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl	479	Qy	839	eAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnPr	859
Db	1438	TGAGCCAGGCGAGCTGCTATGAGGAGTACTCAAGTACTCTGCTGATCATCTCCGAAAGC	1497	Db	2518	CGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTGGCTACATTAAGAATCC	2577
Qy	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499	Qy	859	oTyrAsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGlyGlnG1	879
Db	1498	AGCCCGAAGCTGCGCCAGGTCTCTAGGGCTATAGGGCTGCGGGCTGGCTGTCTAGCAG	1557	Db	2578	CTACAACATCTTTGATGTGTGTCATGTGTGTCATCAGTGTGTGGAGATTTGGGCCACGA	2637
Qy	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519	Qy	879	nglyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr	899
Db	1558	CCCAAGTGGCCGTAGTGGCGAGGAGCCCGCCAGCCAGTGGCAGTGCATCGCTCACACCG	1617	Db	2638	GGGAGGTGGCTGTGCTGCTGCGGACCTTCGCGCTGATCGGGTGTGTAAGCTGGTGGC	2697
Qy	519	gArgLeuSerValHisIleuValHisHisHisHisHisHisHisHisHisHisHisLe	539	Qy	899	gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl	919
Db	1618	TCGTCTGTCTCCACCACCTGGTCCACCACCATCCACCATCCACCATCCACCTACCACT	1677	Db	2698	CTTCTCGCGGCCCTGCAGCGCCAGCTCGTGTGCTCATGAAGACCATGGACCAACGTGGC	2757
Qy	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAlaAs	559	Qy	919	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	1678	GGGTAATGGGAGCTCAGAGTTCCCGGGCCAGCCAGAGATCCAGGACAGGGATGCCAA	1737	Db	2818	CTTTGGTTGCAAGTTCCGATCTGAAACGGGATGGGACACGTTGCCAGACCGGAAGATTT	2877
Qy	559	nglySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr	579	Qy	939	eAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAs	959
Db	1738	TGGGTCTCGCGGCTCATGCTACCAACACCTCTACACCCACTCCCTCTCGGGGCGCTCC	1797	Db	2878	CGACTCCCTGCTCGGGCCATCGTCTCTTTTTCAGATTCTGACTCAGGAAGACTGGAA	2937
Qy	579	oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr	599	Qy	959	nLysValLeuTyrAsnGlyMetAlaSerThrSerThrPheAlaLeuLysTyrPheIleAl	979
Db	1798	GAGGGTCCGGAGTGTACACAGCTTCTACATGCTGACTGCCACTTTGGAGCCAGTCCG	1857	Db	2938	TAAAGTCTCTACACGGCATGGCTCCACATCGTCTTGGGCTGCTCTTTTACTTCATCGC	2997
Qy	599	gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerG1	619	Qy	979	aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuAlaIleLeuValGluG1	999
Db	1858	TTGCCAGGACCCCTCCAGATGCCATCGGAGGCATCTGTTAGGACTGTGGGTAGTGG	1917	Db	2998	CCTCATGACTTTTGGCAACTATGTGCTCTTAACTGCTGGTGGCCATCTTCTTGTGGAAGG	3057
Qy	619	yLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639	Qy	999	yPheGlnAlaGlu-----	1003
Db	1918	GAAGGTGATCCCACTGTGTACATACAGCCCTCCACAGAGATCTGGAAGGATAAGCACT	1977	Db	3058	ATTCCAGGACAGAGAAATCGGCAACCGGAAGATGCGAGTGGACAGTTAAGCTGTATTCA	3117
Qy	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGl	659	Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePh	1016
Db	1978	AGTGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCCTCACAGCTTCAACATCCCACTGG	2037	Qy	3118	GCTGCTGTCAACTCTCAGGGGGAGATGCCAAAGTCTGAGTCTGAGCGCTGATTCTT	3177
Qy	659	yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe	679				

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1745	nLeuGlyLeuLeuPheMetLeuLeuPhePhePheAlaAlaLeuGlyValGluLeuPh	1765		Qy
5398	CCTGGGACCTTCCTCATGTTATTTGTTTTCATCTTTCAGCTCTGGCGGTGGAGCTCTT	5457		Db
1765	eGlyAspLeuGluCyAspGluThrHiProCyGluGlyLeuGlyArgHisAlaThrPh	1785		Qy
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5518	TAGAACTTTGGPATGGCCCTTTTCACCCCTCTTCAGAGTCTCCACTGGTGACACTGGAA	5577		Db
1805	nGlyIleMetLeuAspProSerArgAspCyAspGlnGluSerThrCysTyrAsnThrVa	1825		Qy
5578	TGGTATTATGAAGACACACCTCGGGACTGTGACAGGAGTCCACTGTCTACAACACTGT	5637		Db
1825	IleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVa	1845		Qy
5638	CATCTCCCTTACTACTTGTGTCTGTGTGACGGCCCAAGTTTGCTGTGCTCAAGCT	5697		Db
1845	IValIleAlaValLeuMetIleHisLeuGluGluSerAsnLysGluAlaLysGluAla	1865		Qy
5698	GGTCATAGCTGTGCTGATGAAGCACCTGGAAGAAACCAACAAAGAGGCCAAGAGAGGC	5757		Db
1865	aGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnProHisSerPr	1885		Qy
5758	CGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCGCCGAGCCCACTCCCC	5817		Db
1885	oLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLy	1905		Qy
5818	GCTGGGAGACCCCTTCTCTGGCCGGGTGGAGGGTGTCAACAGTCTGTGACAGCCCTAA	5877		Db
1905	sProGlyAlaProHisThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHi	1925		Qy
5878	GCCTGGGGCTCCACACACCATGCGCCCATTTGAGACAGCCTCGGGCTTCTCCCTTGAGCA	5937		Db
1925	sProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh	1945		Qy
5938	CCCCACAGATGTATCCCAACCCGAGAGGTGCCAGCTCCCTTAGGACACAGCTGTGTGAC	5997		Db
1945	rValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysAr	1965		Qy
5998	TGTGAGGAAGTCTGGTGTGACGGAGCGCATCTCTGCCCAATGACAGCTACATGTGCCG	6057		Db
1965	sAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGl	1985		Qy
6058	CAATGGGAGACTGCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTCCCCAAGGCCCA	6117		Db
1985	nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLe	2005		Qy
6118	GTACGGCTCCACTTGTCCGTTCCTTCCCAACACAGACACAGCTGCAATCTTACAGCT	6177		Db
2005	uProLysAspValHisTyrLeuLeuGlnProHisGlyValaProThrTrpGlyAlaIlePr	2025		Qy
6178	TCCCAAGATGTGCACTATCTGCTCCAGCTCATGGGGCCCCCACTGGGGCGCCATCCC	6237		Db
2025	oLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAl	2045		Qy
6238	TAAACTACCCCACTGGCGGCTCCCTCTGGCTCAGAGGCTCTCAGGGCGCCAGGAGC	6297		Db
2045	AlaArgThrAspSerLeuAspValGlnGlySerArgGluAspLeuLeuSerG1	2065		Qy
6298	AATAAGGACTGACTCCCTGGATGTGAGGGCTTGGTAGCCGGGAAGACCTGTGTGAGA	6357		Db
2065	uValSerGlyProSerCysProLeuThrArgSerSerPheThrGlyGlySerSerI1	2085		Qy
6358	GGTGAGTGGGCCCTCTCTGCTGCTGACCCGGTCTCATCTTCTGGGGCGGGTGGAGAT	6417		Db
2085	eGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAl	2105		Qy

XX This sequence represents the coding region for a rat T-type voltage-gated
PS calcium (Ca) channel alpha-1-G designated rCav1.2. Voltage gated channels
XX are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6762
Score: 11798.00 Matches: 2250
Percent Similarity: 99.78% Conservative: 3
Best Local Similarity: 99.78% Mismatches: 2
Query Match: 98.09% Indels: 0
DB: 2 Gaps: 0

US-09-611-257A-24 (1-2287) x AAX83485 (1-6762)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGGACGAGGAGGAGTGGAGCGCGCGCGGAGGAGTGGAGGAGCGCGGAGTTCACGC 61
QY 54 SerSerThrThrCysProGlyProGlyVala-AlaGlyVala-GlySerThrGluLysAspP 73
DB 62 AGCTCAACGACCTGTCGGGGGCGGGGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGG 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProGlyProAlaLeuAlaProValValP 93
DB 122 CGGCGAGCGCGGAGTCCGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 181
QY 93 hePheThrLeuSerGlnAspSerArgProArgSerThrCysLeuArgThrValCysAsnNP 113
DB 182 TCTTCTACTTGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 241
QY 113 roTrpPheGluArgValSerMetLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 133
DB 242 CGTGGTTCGAGCGAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
QY 133 heArgProCysGluAspAlaCysAspSerGlnArgCysArgileLeuGlnAlaPheA 153
DB 302 TCAGGCGCGTGTGAGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 153 sphaspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
DB 362 ATGACTTCACTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
QY 173 lePheGlyLysLysCysThrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
DB 422 TCTTTGGAGAGAAATGTACTTGGAGACACTTGGAAACCGGCTTGACTTTTCACTGTCA 481
QY 193 leAlaGlyMetLeuGluTySerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
DB 482 TTGCAGGAGTGTGAGTATTTGCTGAGCTGACCTGCGAGAACGTCAGCTTCTCCGAGTCA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
DB 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACCGGTGCGGAGCATGCGATTCTCG 601

QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuLeuLeuLeu 253
DB 602 TCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGCTCCTGCTGCTGCTGCTGCT 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuLeuLeuLeuLeu 273
DB 662 TCTTTTTCATCTTGTGGCATGCTGGGCGTCCAGCTGTGGGAGGAGGAGGAGGAGGAGGAG 721
QY 273 yPheLeuProGluLeuAsnPheSerLeuProLeuSerValAspLeuLeuLeuLeuLeuLeu 293
DB 722 GCTTCTCTCCCGAGAACTTCCAGCTTCCCTTCCCTGAGCGGGAGCTGGAGCCCTTAT 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
DB 782 CAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyG 333
DB 842 CTTGACAGGAGTGTGCCACACTGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 901
QY 333 spTyrGluThrThrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTrpTyrT 353
DB 902 ACTATGAGACCTATAACAGTTCAGCAACACCACTGCTGCTCACTGGAACAGTACTATA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
DB 962 CCAACTGCTCTGGGCGGAGCACACCCCTTCAAGGCGCCATCACTTTTGACAACTTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
DB 1022 GCTATGCTGGATCGGCATCTTCCAGTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAG 1081
QY 393 yrPheValMetAspAlaHisSerPheThrAsnPheIleTyrPheIleLeuLeuLeuLeu 413
DB 1082 ACTTCTGTAATGGAGGCTCACTCTCTTACAACTTCACTACTTCTTCTTCTTCTTCT 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT 433
DB 1142 TGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
DB 1202 CCAACAGCGGAGGAGTCACTGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
DB 1262 GCACCTTGGCAAGCTTCTCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValA 493
DB 1322 TGTACATCTCTCCGAAAGCAGCCGAGGCTGGCCCGGAGGCTCTAGGGCTATAGGCGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
DB 1382 GGGCTGGGCTGCTCAGCAGCCAGTGGCGGCTAGTGGGAGGAGGAGGAGGAGGAGGAG 1441
QY 513 erCysThrArgSerHisArgLeuSerValHisLeuValHisLeuValHisLeuValHis 533
DB 1442 GCTGCACTGCTCACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
QY 533 iShiShiShiThrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
DB 1502 ACCATCACCACTACCACTGGGTAATGGGAGCGCTCAGAGTTCCTCCCGGCGCCAGCA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
DB 1562 TCCAGGACAGGAGTGGCAATGGGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1621
QY 573 hrProSerGlyGlyProProArgGlyValaGluSerValHisSerPheThrHisLeuAspC 593
DB 1622 CTCCTCTTGGGGGCGCTCCGAGGGGCTGCGAGGCTGTGTACACAGCTTCTACATGCTG 1681
QY 593 yShiLeuGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerG 613

1682	Db	GCACCTTGGAGCAGTTCGTTGCCAGGACCCCTCCAGATGCCATCGGAGCATCTG	1741
613	Qy	lyArgThrValGlySerGlylysValTyrProThrValHisThrSerProProGluI	633
1742	Db	GTAGGACTGTGGTAGTGGGAAGGTGTACCCCACTGTGCATACGAGCCCTCCACCAAGA	1801
633	Qy	leLeuIysAspIysAlaIleuValGluValAlaProSerProGlyProProThrLeuThrS	653
1802	Db	TACTGAAGGATAAAGACACTAGTGGAGGTGGCCGCCAGCCCTGGGCCCCCACTCACC	1861
653	Qy	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
1862	Db	GCCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCAACAAGCTCCTGGAGACACAG	1921
673	Qy	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
1922	Db	CGGAGCCTGCCATAGCTCTCGAAATCTCCAGCCCTTGTCTCAAGGACACAGTGGAG	1981
693	Qy	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyValaGlyGluProGluSerA	713
1982	Db	CCTCGGGCCGGACAGTGTCTCTACTGTGCTCCGCGACAGGAGGAGGACGAGTCCG	2041
713	Qy	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
2042	Db	CTGACCATGTCATGCCCTGACTCAGACAGGAGGAGCTGTGTATGATTCACAGACGCTC	2101
733	Qy	lnHisSerAspLeuAraAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
2102	Db	AGCACTGACCTCCGGGATCCCAAGCCGCGGCGGACAGCGGAGCTGGGCCACAGATG	2161
753	Qy	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIlysIleV	773
2162	Db	CAGAGCCTAGTTCGTGCTGCTTCCTGAGGCTGATCTGTGCACACATTCGCGAAGTCG	2221
773	Qy	alAspSerIlyTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
2222	Db	TAGATAGCAAAATACTTTGGCCGGGAATCATGATCCCATCCCTGTGTCAATCAGCTC	2281
793	Qy	erGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
2282	Db	TGGGATCGAGTACCAGCAGCAGCCGAGGAGCTCACCAGCCCTGGAAATCAGCAACA	2341
813	Qy	leValPheThrSerLeuPheAlaLeuGluMetLeuIlysLeuLeuValTyrGlyProp	833
2342	Db	TCGTCTTACCAGCCTTCCTCCCTTGAGATGCTGTGAATCTGTGTGTGTGTGTGTGT	2401
833	Qy	heGlyTyrIleIysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT	853
2402	Db	TTGGCTTACATTAAGAAATCCCTACCAATCTTTGATGTGTGTGTGTGTGTGTGTGT	2461
853	Qy	rpGluIleValGlyGlnGlnGlyLysLeuSerValLeuAraGlyThrPheArgLeuMetA	873
2462	Db	GGGAGATGTGGCCAGCAGGAGGTGGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGT	2521
873	Qy	rgValLeuIlysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValMetL	893
2522	Db	GGGTGTGAAGTGTGGCTTCTTCCCGGCCCTTCGAGCCAGCTGTGTGTGTGTGTGT	2581
893	Qy	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhePheS	913
2582	Db	AGACCATGGACACAGTGGCCACTTCTGTCATGCTCTCATGCTGTGTGTGTGTGTGT	2641
913	Qy	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAraGlyAspThrL	933
2642	Db	GCATCTCTGGGCATGCATCTCTTGTGTGCAAGTTCGCATCTGAACGGGATGGGAC	2701
933	Qy	euProAspAraGlyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
2702	Db	TGCCAGACCGGAGAAATTTCCGACTCCCTGCTCTGGGCCATCTGTCTCTTTCAGAT	2761
953	Qy	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
2762	Db	TGACTCAGGAGACTGGAATAAAGTTCCTCTACAAACGGCATGGGCTCCACATCTCTT	2821
973	Qy	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993
2822	Db	CTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACTGCT	2881
993	Qy	alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP	1013
2882	Db	TGGCCATTCCTTTGGNAGGATTCAGGAGGAGGAGATGCCAACAGTCTGAGTCAAGC	2941
1013	Qy	roAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV	1033
2942	Db	CTGATTTCTTTTCGCCACAGTGTGATGTGGGACAGAAAGCGCTTGGCCCTGG	3001
1033	Qy	alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT	1053
3002	Db	TGGCTTTGGGAGAACACGGGAACCTACGAAAGAGCTTTTGGCCACCTCATCATCATA	3061
1053	Qy	hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG	1073
3062	Db	CGGCTGGCACCAATGTCCACCCCAAGAGCTCCAGCACAGGTTGGGGGAAGCACTGG	3121
1073	Qy	lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisG	1093
3122	Db	GCTCTGCTCTCCAGCGTACCAGTAGCAGTGGGTCCGCTGAGCTGGAGCTGCCACCATG	3181
1093	Qy	luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS	1113
3182	Db	AGATGAATGTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGGAGTGGCGCAAGCA	3241
1113	Qy	erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIysArgA	1133
3242	Db	GCTGGACCAAGCGCTCCAGCAGGAAACAGCTGGGGCCGGGCCCCAGCCCTTAAGACGA	3301
1133	Qy	rgSerProSerGlyGluArgArgSerSerLeuSerGlyGlyGluGlnGlnSerGlnAspG	1153
3302	Db	GGAGCCCGAGCGGAGCGGAGGTCCCTGCTGTCTGAGAGGGCCAGGAGTCAAGAGT	3361
1153	Qy	luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
3362	Db	AGGAGGAAATTCAGAAAGAGACCGGGCCAGCCAGCAGCAGTGAACCTGCCACAGGG	3421
1173	Qy	lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG	1193
3422	Db	GTTCTCTGAAAGTGTAGGCCAAGAGTTCCTTTGACCTGCTGACACTCTGCAGTCCCG	3481
1193	Qy	lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL	1213
3482	Db	GGCTGACCGCACACCCAGCGCGGAGCTGTGCTCTGAGCAACCAAGACTGTAATGGGA	3541
1213	Qy	ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA	1233
3542	Db	AGTCCGCTTTCAGGGCTTTGGCCCGCACCTTCAGAGACTGTATGACCCCACTGATGGG	3601
1233	Qy	spAspAspAsnAspGluGlyAsnLeuSerLysGlyArgIleGlnAlaTrpValArgS	1253
3602	Db	ATGATGACAAATGATGAGGGAATCTGAGCAAAAGGAAACGACATACAAAGCTTGGT	3661
1253	Qy	erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG	1273
3662	Db	CCCGGCTTCTGTGCTTGGCCGAGCGAGATTCCTGTGTGGCCCTATATCTTCTCTCTC	3721
1273	Qy	lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV	1293
3722	Db	AGTCAGAGTTTCTCTCTCTGTGTCCCGGATCATCCACCAGATGTTTGTGACCATGTG	3781
1293	Qy	alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP	1313
3782	Db	TCCTCGTTCATCTCTTCTCACTGTGTATCACCATCGCTATGGAGGGCCCCCAAAAT	3841
1313	Qy	roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL	1333
3842	Db	CCCAACAGCGCTGAGCGCATCTTCTTGACCCCTCTCCAACTACATCTTCCAGCGAGT	3901

1333 euAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrL 1353
1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLleSerValIleAspIleL 1373
1362 TGCGCAGCAGCTGGAATGTCTCGACGGCTTGTGTGTCTCATCTCCGTTCATCGACATCC 4021
1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
4022 TGTCTCTCATGGTCTCCGACAGCGGCACCAAGATCCCTTGGCATGCTGAGGGTCTCGGC 4081
1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
4082 TGCTGGGACCTCGCTCCACTCAGGGTCATCAGCGGGCCAGGACCTGAAGCTGGTGG 4141
1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaP 1433
4142 TAGAGACTCTGATGTCATCCCTCAAAACCCATTCGCAACATGTGGTCAATTTGCTGTGCCT 4201
1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
4202 TCTTCATCATTTTGGAAATTTCTCGGGTGCAGCTCTTCAAAGGAAAGTTCTTCGTGTGC 4261
1453 lncGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473
4262 AGGGTGAGGACACCGAAGACATCACTAACAAATCCGACTCGCTGAGGCAGCTACCGAT 4321
1473 rpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
4322 GGGTCGGCAACAAGTCAACCTTTGACAACTGGGCCAGGCTCTGATGTCTCTTTGTGC 4381
1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
4382 TGCCCTCCAAAGATGGTGGTGTGACATCATGTATGATGGCTGGATGTCTGGGTGTGG 4441
1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
4442 ATCAGCAGCCCATCATGAACACACACCCCTGGATGCTGTCTATCTCTCTCTCTCTCC 4501
1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
4502 TCATCGTGGCTTCTTTGCTGAAACATGTTGTGGCGTGGTGGTGGAGAACTTCCATA 4561
1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgA 1573
4562 AGTGCAGACAGCACCCAGGAGGAGGAGCGGCGGCGGTGAGGAGAAAGCGACTACGGA 4621
1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProT 1593
4622 GGCTGGAGAAAGAGAGAGATAGAGAGAGAGATGGCCGAGGAGCCAGTGCAGCCCT 4681
1593 yrTrpSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL 1613
4682 ACTACTCTGACTACTCGAGATTCGGCTCTCTGTCCACCACTGTGTACCAGCCACTACC 4741
1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633
4742 TGGACCTCTTCATCATCTGGTGTCTCGGGTGAACCGTGGTCACTATGGCCATGGAAACAT 4801
1633 yrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1653
4802 ACCAGCAGCCCGAGATCTCGAGCGGCTCTGAAGATCTGCAATTTACATCTTTACCGTCA 4861
1653 lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgPhePheGlnA 1673
4862 TCTTTGTCTTTGAGTCAGTTTTTCAAACTTGTGGCTTTTGGCTTCGGCCGTTTCTTCCAGG 4921
1673 spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693
4922 ACAGGTGGAAACCGACTGGACTGGCTATTGTGTCTTGTCTTCATCATGGGCATCACACTGG 4981

1693 luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713
4982 AGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCACCATCATCTCGTATCATGAGG 5041
1713 alLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733
5042 TGCTCCGCAATGTCTGAGTCTTGAAGCTGTGAAGATGGCTGTGGGCATCGCGGCATGC 5101
1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
5102 TGCACACGGGTGATGACAGGCCCTGCCCCAGGTGGGAACTTGGGACTTCTCTTCATGTTAT 5161
1753 euPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773
5162 TGTTTTTTCATCTTTGAGCTCTGGGCTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGA 5221
1773 hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
5222 CACACCTTGTGAGGGCTTGGGTGGCATGCCACCTTTAGGAACCTTTGGTATGSCCTTTC 5281
1793 euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813
5282 TGACCTCTTTCGAGTCTCCACTGGTGAACAACCTGGAATGGTATTATGAAGGACACCTTCC 5341
1813 rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS 1833
5342 GGGACTGTGACCGAGGAGTCCACCTGCTACACACATGTCATCTCTCCCTATCTACTTTGTGT 5401
1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853
5402 CCTTCGTGTGACGGCCAGTTTGTCTGCTGCTCAACGCTGGTTCATAGCTGTGCTGATGAAGC 5461
1853 isLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluL 1873
5462 ACCTTGAAAGAAAGCAACAAAGAGGCCCAAGAGAGGCCGAGCTCGAGGCCGAGCTGAGC 5521
1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP 1893
5522 TGGAGATGAAGACGCTCAGCCCGACCCCTCTCCCGCTGGGCGCCCTCTCTCTGCG 5581
1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
5582 CCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTTAAGCGCTGGGGCTGCCACACACCTG 5641
1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933
5642 CCACATTTGGAGCAGCTCGGGCTTCTCCCTTGAGCACCCTCCAGATGGTATCCCAACCCCG 5701
1933 luGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerA 1953
5702 AGGAGGTGCCAGTCCCTTAGGACACAGACTGCTGACTGTGAGGAAGTCTGGTGTGAGCC 5761
1953 rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS 1973
5762 GGAACGCACTCTCTGCCCAATGACAGTACATGTGCGCAATGGGAGCACTGTCTGAGAGAT 5821
1973 erLeuGlyHisArgGlyTrpGlyLeuProLysValGlnSerGlySerIleLeuSerValH 1993
5822 CCTTAGACACAGGGGCTGGGGCTCCCCAAAGCCCGAGCTCCATCTTGTCTCGTTC 5881
1993 isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL 2013
5882 ACTCCCAACACGACAGACACAGCTGCATCTCTACAGCTTCCCAAGATGTGCACTATCTGC 5941
2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgS 2033
5942 TCCAGGCTCATGGGGCTCCACCTGGGGGGCCATCCCTTAACTACCCCACTGGCGCT 6001
2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053
6002 CCCCTTGGCTCAGAGGCTCTCAGGCGCCAGCAGCAATAGGACTGACTCTCCTGGATG 6061
2053 aiGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073

Db	6062	TGCAGGGCCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGTGAGTGGGGCCCTCCTCGCCCTC	6121
Qy	2073	euthrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI	2093
Db	6122	TGACCCGGTCCCTCATCCTTCTGGGGGGGTTCAGAGATCCAGGTGACAGCGTTCGGCA	6181
Qy	2093	leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS	2113
Db	6182	TCCAGAGCAAGTCTCCAAAGCATCCGGCTGCGACCCCTTGCACAGCCCTCGCAACCCA	6241
Qy	2113	erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT	2133
Db	6242	GCTTGGGCCAAGGACCTTCAGAGACCCAGAAAGAGCTTAGAGCTGGACACGGAGCTGAGCT	6301
Qy	2133	rpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL	2153
Db	6302	GGATTTCAGAGACCTCCTTCCAGCAGCCAGGAAGACCCCTGTTCCACGGAGACCTGA	6361
Qy	2153	ysLysCysTyrSerValGluThrGlnSerCysArgArgProGlyPheTrpLeuAspG	2173
Db	6362	AGAAAGTGCTTACAGTTAGAGACCCAGAGCTGCAGGCGCAGCGCTTGGGTCTGGCTAGATG	6421
Qy	2173	luGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuC	2193
Db	6422	AACAGCGGAGACATCCATTGCTGTACGTCTGGACACGGCTCCCAACCCCGCTAT	6481
Qy	2193	ysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysL	2213
Db	6482	GTCCNAGCCCTCAAGCTCGGGGGCCAACTCTTGGGGTCTCTGGAGCGCGCTAAGA	6541
Qy	2213	ysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProp	2233
Db	6542	AAAAACTCAGGCCACCCCAAGTATCTATAGACCCCGCCGGAGCCAGGGCTCTCGCCCC	6601
Qy	2233	roCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProS	2253
Db	6602	CATGCAGTCTGGTGTCTGCTCAGGAGGCGCGCGCCAGGTGACTCTTAAGGATCCCT	6661
Qy	2253	erValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuS	2273
Db	6662	CGGTCTCAGGCCCCCTTGACAGCAGCGTGTCTACCTCTCCCAAGAAAGACACGCTGA	6721
Qy	2273	erLeuSerGlyLeuSerSerAspProThrAspMetAspPro	2286
Db	6722	GNCTCTGTGTGTCTTCTGACCCCAACAGACATGGACCC	6762

RESIST 5

A83021	
AAK83487	
ID	AAK83487 standard; cDNA; 6816 BP.
XX	
XX	AAK83487;
XX	
XX	07-DEC-1999 (first entry)
DT	
XX	Rat T-type voltage-gated Ca channel alpha-1-G (rCavTic) cDNA.
DE	
XX	
XX	Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW	Accession: AAK83487; screen: drugg: cardiomyopathy; epilepsy; ds.

XX WPI; 1999-394972/33.
DR P-PSDB; AA14592.
XX
XX New T-type voltage-gated calcium channels.
XX
XX Disclosure; Page 85-94; 138pp; English.
PS
XX This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCav1.2. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AA83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AA14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods can also be disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
XX Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;
SQ

Alignment Scores:	Length:	6816
Pred. No.:	Matches:	0 2248
Score:	Conservative:	11767.00 5
Percent Similarity:	Mismatches:	98.90% 20
Best Local Similarity:	Indels:	98.90% 1
Query Match:	Gaps:	97.83% 2

US-00-511-257A-24 (1-2287) x AAX83487 (1-6816)

34	TtpThrArgArgMetGluAraAlaProArgSerArgAspSerProValAlaSerArg	53	
Db	2	TGGACGAGGAGGAGATGGAGCGGGCGCGAGAGATCGGAGCAGCCCGGTAGCTTCACGC	61
QY	54	SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluIysAspP	73
Db	62	AGCTCAAAGCACTGTCGGGGGCGGGGCGGAGCGGGCGGGGTCGACGGAAAGGACC	121
QY	73	roGlySerAlaAspSerGluAlaGluClyLeuProTyrProAlaLeuAlaProValValP	93
Db	122	CGGGCAGCGCGACTCCGAGCGGAGGGGTGCGGTACCCGGCGCTAGAGCCCGGTGGT	181
QY	93	hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	113
Db	182	TCCTTACTTTGAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAAAC	241
QY	113	roTrrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP	133
Db	242	CGTGGTTCGAGCGAGTCAGTATGCTGGTCACTTCTTCTCAACTGTGTGACTCTGGGTATGT	301
QY	133	heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA	153
Db	302	TCAGGCGGTGTGAGGACATTCGCTGTGACTCCGAGCCGTCCGGATCTCGAGCCCTCG	361
QY	153	spAspPheIlePheAlaPheAlaValGluMetValValIysMetValAlaLeuGlyI	173
Db	362	ATGACTTTCATCTTTGGCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCTTCGGCA	421
QY	173	lePheGlyIysIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI	193
Db	422	TCITTTGGAGAAATGTTTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATGTCA	481
QY	193	leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
Db	482	TTGCAGGGATGCTGGAGTATTTCGTGGACCTCGAGAACGTTCAGCTTCTTCGCAGTCAGGA	541

QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
DB 542 CAGTCCGTGTCTGGAGCCGCTCAGGGCCATTAAACCGGGTGGCCAGCATCGCATCTCG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAenValLeuLeuLeuCysPhePheV 253
DB 602 TCACATTACTGCTGGACACCTTGCTATGTGTGGCAACGTCCTGCTGCTCTGTTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
DB 662 TCATTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGAGGACTGCTTCGCAACCGGT 721
QY 273 ysPheLeuProGluAAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
DB 722 GCTTCCTCCCGAAGACTTCAGCCTCCCTGAGCTGGACCTGGAGCCCTATTACAGA 781
QY 293 hrGluAenGluAAspGluSerProPheIleCysSerGlnProArgGluAAsnGlyMetArgS 313
DB 782 CAGAGATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGAT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA 333
DB 842 CCTGCAGAGGTGTGCCACACTGCTGGGGAAGCGGTGGGCCACCCCTGCAGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
DB 902 ACTATGAGACTATAACAGCTTCAGCAACACCACCTGTGTCACTGGAAACAGTACTATA 961
QY 353 hrAenCysSerAlaGlyGluHiAAsnProPheIysGlyAlaIleAAsnPheserAsnIleG 373
DB 962 CCAACTGCTCTGGGGGGAGACACAAACCCCTTCAAAGCGCCATCAACTTTGACAAACATTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
DB 1022 GCTATGCTCGATCGCCATCTTCAGGTCTATCACTGGAGGGGTGGGTGCACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
DB 1082 ACTTCGTAAAGAGCTCACTCTCTTCAAACTTCACTACTTCACTTCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
DB 1142 TGGGCTCTCTTTCATCATCAACCTGCTGCTGGTGGTGAATTGCCACGAGTTCTCCGAGA 1201
QY 433 hrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas 453
DB 1202 CCAAAACAGCGGAGAGTCAGCTGATGCGGGAGCAGCGGTACGATTCCTGTCCAATGCTA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
DB 1262 GTACCTTGGCAGAGCTTCTTGAGCCAGGAGCTGCTATGAGGAGTACTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
DB 1322 TGTACATCTCCGAAAAGAGCCGAGGCTGGCCCAAGTCTCTAGGGCTATAGGCGTGC 1381
QY 493 rgaAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
DB 1382 GGGCTGGGCTGCTCAGCAGCCCACTGGCCCGTAGTGGGCGAGGAGCCCGCCAGCTGGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
DB 1442 GCTGCATCGCTCACACCGTGTCTGTCTGTCACCACTGGTCCACCATCACCACCC 1501
QY 533 isHisHisHisTyrHisLeuGlyAAsnGlyThrLeuArgValProArgAlaSerProGluI 553
DB 1502 ACCATCACCACTACCACTGGGTAATGGGAGCTCAGAGTTCCCGGCGCCAGCCACAGA 1561
QY 553 leGlnAspArgAspAlaAAsnGlySerArgArgLeuMetLeuProProSerThrProT 573
DB 1562 TCCAGGACAGGGATGCCAATGGGTCTCGCGGCTCATGTACCAACCAACCCCTCTACACCCA 1621

QY 573 hrProSerGlyGlyProProArgGlyValaGluSerValHisSerPheTyrHisAlaAspC 593
DB 1622 CTCCTCTCGGGGGCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGACT 1681
QY 593 yshiLeuLeuProValArgCysGlnAlaProProArgCysProSerGluAlaSerG 613
DB 1682 GCCACTTGGAGCCAGTCCGTTGCCAGCACCCCTCCAGATGCCCATCGGAGCATCTG 1741
QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
DB 1742 GTAGGACTGTGGGTAGTGGNAGGTGTACCCCACTGTGCATACAGCCCTCCACAGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValaProSerProGlyProProThrLeuThrS 653
DB 1802 TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCAGCCCTGGGGCCCCCACCCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
DB 1862 GCTTCAACATCCCACTGGGCCCTTCAGCTCCATGCACAAGCTCTCGGAGACACAGATA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
DB 1922 CGGAGCCTGCCATAGCTCTGCAAAATCTCCAGCCCTGCTCCAGGCGACAGAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
DB 1982 CCTGGGGCGGAGACAGTTGTCCCTACTGTGCCGCGAGGAGGAGGAGGAGGAGTCCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
DB 2042 CTGACCATGTGATGCTGCTGACTCAGACAGCGAGGCTGTGTATGAGTTTCCACAGAGCCTC 2101
QY 733 lnhIserSerLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
DB 2102 AGCACAGTAGACTTCCGGGATCCCCAGCCGCGGCGAGGAGGAGGAGGAGGAGGAGGAG 2161
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
DB 2162 CAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCGGAAGATCG 2221
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
DB 2222 TAGATAGCAAAATCTTTGGCCGGGAATCATGATCGCCATCTCTGGTCAATACATCAGCA 2281
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
DB 2282 TGGCATCGAGTACACAGAGAGCCGAGGAGCTACCAACGCCCTCGAAATCAGCAACA 2341
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProP 833
DB 2342 TCCTCTTACCAGCCTCTTCGCCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCT 2401
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
DB 2402 TTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCAATTGTGGTTCATCAGTGTG 2461
QY 853 rpGluIleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetA 873
DB 2462 GGAGATTTGGGCCAGAGGAGGGTGGCTGTGGTGTGCTGGGAGCTTCGCGCTGATGC 2521
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
DB 2522 GGGTGTGAAGCTGGTGGCTTCTGCCGCGCTTCGAGCGCCAGCTGCTGTGGTCTCATGA 2581
QY 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
DB 2582 AGACCATGGACAACAGTGGCCACCTTCTGCATGTCTCTCATGTCTTCTTCTTCTTCA 2641
QY 913 erIleLeuGlyMetHisLeuPheGlyCysPheAlaSerGluArgAspGlyAspThrL 933
DB 2642 GCATCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGACACGT 2701
QY 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953

Db	2702	TGCCAGACCGGAAGAAATTCGACTCCCTGCTGGCCCATCGTCACTGCTTTTCAGATTG	2761	Db	3782	TCTCGTCATCATCTTCTCAACTGTATCAACCATCGCTATGAGCGCCCAAAATTGACC	3841
Qy	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpA	973	Qy	1313	roHisSerAlaGluArgIlePheLeuThrIleuSerAsnTyrIlePheThrAlaValPheL	1333
Db	2762	TGACTCAGGAAGACTGGAATAAAGTCCCTACACCGGCATGGCTCCACATCGCTTTGGG	2821	Db	3842	CCACACGCGTGAAGCATCTTCTGACCTCTCCAACTACATCTTCACGCGAGCTTTTC	3901
Qy	973	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993	Qy	1333	euAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrL	1353
Db	2822	CTGCTCTTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGTCTCTTAACCTGCTGG	2881	Db	3902	TAGCTGAATGACAGATGAGGTGGTGGCACTGGCTGGTGGTCTTTGGGAGAGCGCTACC	3961
Qy	993	alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP	1013	Qy	1353	euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL	1373
Db	2882	TGGCCATTCTTGTGGAAGATTCCAGCGAGAGGAGATGCCACCAAGCTGTAGTCAGAGC	2941	Db	3962	TGGCAGCAGCTGGATGTCTGACGGCTTGTGTGCTCATCTCCGTATCGATCATCC	4021
Qy	1013	roAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV	1033	Qy	1373	euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL	1393
Db	2942	CTGATTTCTTTTCGCCCAAGTGTGATGGTGATGGGGACAGAAAGAGCGCTTGGCCCTGG	3001	Db	4022	TGCTTCCTCATGGTCTCCGACAGCGGCACCAAGATCTTGGCATGCTGAGGGTGTGGCGC	4081
Qy	1033	alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT	1053	Qy	1393	euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV	1413
Db	3002	TGCTTTTGGAGAACACCGCGAACTACGAAAGAGCCCTTTTGGCACCCCTCATCATCCATA	3061	Db	4082	TGCTGGCGACCTTGGTCCACTCAGGGTCTATCAGCGCGGCCAGGGACTGAAGCTGGTGG	4141
Qy	1053	hrAlaAlaThrProMetSerHisProLysSerSerThrGlyValGlyGluAlaLeuG	1073	Qy	1413	alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaP	1433
Db	3062	CGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGACAGGTGGGGGAGCACTGG	3121	Db	4142	TAGAGACTCTGATGTCTATCCCTCAACCCCATTTGGCAACATTTGGTGTCTTGTGCTGCT	4201
Qy	1073	lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisG	1093	Qy	1433	hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG	1453
Db	3122	GCTCTGCTCTTCGACGTACAGTAGCAGTGGGTCCGCTGAGCTGGAGTGGCCACCATG	3181	Db	4202	TCTTCATCATTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAAGTCTTCTCGTGTGTC	4261
Qy	1093	luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS	1113	Qy	1453	lnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT	1473
Db	3182	AGATGAATGTCCGCCAAGTCCCGCAGCTCCCGCACAGTCTCGAGTGGCGGAAGCA	3241	Db	4262	AGGGTGAAGACACACGAGAACATCATTAACAAATCCGACTCGCTGGCTGAGCGCAGTACC	4321
Qy	1113	erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA	1133	Qy	1473	rpValArgHisTyrIleThrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL	1493
Db	3242	GCTGGACGACAGCGCTCCAGCAGGAACACCTTGGCCCGGCCGCCCGCCAGCTAAAGCGGA	3301	Db	4322	GGGTCCGGCAGCAAGTACAACTTTGACAACTTGGCCAGGCTCTCATGTGCTGTTGTGC	4381
Qy	1133	rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGlnAspG	1153	Qy	1493	euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA	1513
Db	3302	GGAGCCCGAGCGGGAGCGAGGTCCCTGTCTGTGAGAGGGCGCAGAGAGTCAAGATG	3361	Db	4382	TGGCTCCCAAGGATGGTGGGTTCACATCATGTATGATGGCTGGATGCTGGGTGGG	4441
Qy	1153	luGluGluSerSerGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173	Qy	1513	spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL	1533
Db	3362	AGGAGGAAGTTCAAGAGAGACCGGGCCAGCCCGAGCGAGCGATCCATCGCCACAGG	3421	Db	4442	ATCAGCAGCCCATCATGAACACCAACCCCTGGATGCTGCTATATCTTCTCTCTCC	4501
Qy	1173	lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG	1193	Qy	1533	euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL	1553
Db	3422	GTTCTTGGACGTGAGGCCAAGATTCTTTGACCTGCTGACACTCTGCAGGTGCGCG	3481	Db	4502	TCTCGTGGCTTCTTGTCTGAAACATGTTTGTGGGGTGGTGGTGGAGAACTTCCATA	4561
Qy	1193	lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAncGlyL	1213	Qy	1553	ysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgA	1573
Db	3482	GGCTCACCGCACAGCCAGCGCGAGCTCTGCTCTGAGCACCAAGACTGTAAATGGCA	3541	Db	4562	AGTGCAGACAGCACCGAGGAGGAGGCGCGCGGTGAGGAGAACCCACTACCGA	4621
Qy	1213	ysSerAlaSerGlyArgGluAlaArgThrLeuArgThrAspProGlnLeuAspGlyA	1233	Qy	1573	rgLeuLysLysLysArgArgSerLysGlyLysGlnMetAla-----	1586
Db	3542	AGTCGGCTTCAGGGGCTTTGGCCCGCCACCTTGAGGACTGATGACCCCACTGGATGGG	3601	Db	4622	GGCTGGAGAAAAGAGAGAGAGTAAAGAGAACAGATGSCCGATCTAATGTTGGACGATG	4681
Qy	1233	spAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS	1253	Qy	1587	-----GluIleGlnCysLysProTyrTyrS	1595
Db	3602	ATGATGACATCATGATGAGGAAATCTGAGCAAGGGGAAACGACAGACCAAGCTGGGTCA	3661	Db	4682	TAATTGCTTCGGCAGCTCAGCGCTGCGCTGAGAACCCAGTGCAGAGCCCTACTACT	4741
Qy	1253	erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG	1273	Qy	1595	erAspTyrSerArgPheArgLeuLeuValHisLeuCysThrSerHisTyrLeuAspL	1615
Db	3662	CCCGGCTTCCTGCTGTTGCCGAGAGCGAGATCTCTGTGGCGCTATATCTTCTCTCTC	3721	Db	4742	CTGACTACTCGAGATTCGGGCTCTTGTCCACACCTGTGTACCGACCACTACCTGGACC	4801
Qy	1273	lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV	1293	Qy	1615	euPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnG	1635
Db	3722	AGTCAGGTTTCTGCTCTGTTGTCACCGGATCATCACCAAGATGTTTACCATGTGGG	3781	Db	4802	TCITTCATCACTGGTGTTCATCGGCTGAACGTGTGTCTATATGCGCATGGAACATAC	4861
Qy	1293	alLeuValIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP	1313	Qy	1635	lnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheV	1655
				Db	4862	AGCCCCAGATCTCTGGAGCGAGGCTCTGAAGATCTGCAATTTACATCTTTACCGTCACTTTG	4921

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Qy 1655 alPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgT 1675
Db 4922 TCTTTGAGTCAGTTTTCAAACTGTGGCCCTTGGCTTCCGCCGTTTCTTCAGAGCAGGT 4981
Qy 1675 rpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluI 1695
Db 4982 GGAACCAAGCTGCAGCTGGCTATTGTGCTTCTGTCCATCGGCATCACACTGGAGGAGA 5041
Qy 1695 leGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuA 1715
Db 5042 TTGAGGTCAATCTCTGCTGCCCCATCAACCCACCATCCGATCATGAGGTGTCTCC 5101
Qy 1715 rgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisT 1735
Db 5102 GCATTGCTCGAGTCTCGAGCTGTGAAGATGGCTGTGGGATCGCGGCATCTGTGCACA 5161
Qy 1735 hrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
Db 5162 CGGTGATGCAGGCCCTGCCCGAGGTGGGAACCTGGGACTTCTCTCATGTTATTGTTTT 5221
Qy 1755 heIlePheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisP 1775
Db 5222 TCATCTTTGAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACC 5281
Qy 1775 roCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
Db 5282 CTGTGTAGGGCTTGGGTGGCATGCCACCTTTAGAACCTTGTGATGGCTTCTTGACCC 5341
Qy 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspC 1815
Db 5342 TCTTCCGAGTCTCCACTGGTGACAACCTGGAATGTTATTGAAGGACACACCTCCGGGACT 5401
Qy 1815 ysAspGlnGluSerThrCysTrpAsnThrValIleSerProIleTyrrPheValSerPheV 1835
Db 5402 GTGACCAAGGATCCACCTGCTTACAACTGTGCATCTCCCTCATCTACTTTGTGCTTCG 5461
Qy 1835 alLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG 1855
Db 5462 TGCTGACGGCCAGTTTGTGCTGTCAACGTGTGTCATAGCTGTGCTGATGAAGCACCTGG 5521
Qy 1855 luGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLum 1875
Db 5522 AAGAAAGCAACAAAGAGGCCAAGAGGAGGCGGAGCTCGAGGCGGAGCTGGAGCTGGAGA 5581
Qy 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1895
Db 5582 TGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGGCAGCCCTTCTCTGGGCCCGGGG 5641
Qy 1895 alGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisI 1915
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Qy 1915 leGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluLuv 1935
Db 5702 TTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACCGATGTTACCCACCCCGAGGAGG 5761
Qy 1935 alProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrH 1955
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Qy 1955 isSerLeuProAsnAspSerTyrrMetCysArgAsnGlySerThrAlaGluArgSerLeuG 1975
Db 5822 ACTCTCTGCCCAATGACAGCTACATGTGCCCAATGGAGCACTGTGAGAGATCCCTAG 5881
Qy 1975 lyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerG 1995
Db 5882 GACACAGGGCTGGGGCTCCCCAAGCCAGTCAGGCTCCATCTTGTGCTTCACTCCC 5941
Qy 1995 lnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrrLeuLeuGlnP 2015
Db 5942 AACCAGACAGACACCAAGCTGCATCTTCCAAAGATGTGCATATCTGTCTCCAGC 6001
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Qy 2015 roHisGlyAlaProThrTrpGlyValaIleProLysLeuProProGlyArgSerProL 2035
Db 6002 CTCACTGGGGTCCCACTCTGGGGCGCCATCCCTAAACTACCCCACTTGGCGCTCCCTC 6061
Qy 2035 euAlaGlnArgProLeuArgArgGlnAlaIleAlaIleArgThrAspSerLeuAspValGlnG 2055
Db 6062 TGGCTCAGAGGCTCTCAGCGCGCAGCAGCAATAAGGACTGACTCCCTGGATGTGCAGG 6121
Qy 2055 lyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrA 2075
Db 6122 GCCTGGGTAGCCGGGAAGACCTGTGTTCAGAGGTGAGTGGGCCCTCTCTGCCCTCTGACC 6181
Qy 2075 rgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnArgSerGlyIleGlnS 2095
Db 6182 GGTCTCTCATCTTCTGGGGCGGGTTCAGCATCCAGGTGCAGAGCGTTCGGCATCCAGA 6241
Qy 2095 erLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpA 2115
Db 6242 GCAAAAGTCTCAAGCACATCCGCTTGCAGGCCCTTGCAGCGGCTTGCAGAGCTGGG 6301
Qy 2115 laLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIles 2135
Db 6302 CCAAGGACCTCCAGAGACCAGAAAGCAGCTTAGAGCTGGACACGAGCTGAGCTGGATT 6361
Qy 2135 erGlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAspLeuLysLysC 2155
Db 6362 CAGGAGACCTCTTCCAGCAGCCAGGAAGAACCCCTGTTCACACGGGACTTGAAGAACT 6421
Qy 2155 ysTyrrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluAla 2175
Db 6422 GCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGGTCTTGGCTAGATGAACAGC 6481
Qy 2175 rgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProS 2195
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Qy 2195 erProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLysL 2215
Db 6542 GCCCTCAAGCTTCGGGGGCCAACCTCTTGGGGGTCTTGGAGCGCGGCTTAAGAAAAAC 6601
Qy 2215 euSerProSerIleSerIleAspProGluSerGlnGlySerArgProProCysS 2235
Db 6602 TCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAGGCTCTCGGCCCATGCA 6661
Qy 2235 erProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValS 2255
Db 6662 GTCTGTGTCTGCTCAGAGGAGGCGCGCCAGTGACTCTAAGGATCCCTTCGGTCT 6721
Qy 2255 erSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuS 2275
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Qy 2275 erGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6782 CTGTTGTCTTCTGACCCCAACAGACATGGACCCC 6816
RESULT 6
AAx83486
ID AAX83486 standard; cDNA; 6795 BP.
XX
AC AAX83486;
XX
DT 07-DEC-1999 (first entry)
XX
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
OS Rattus sp.
XX
PN W09929847-A1.
XX
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QY	533	isHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
DB	1502	ACCATCACTACCACTGGTAAATGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAGA	1561
QY	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT	573
DB	1562	TCCAGGACAGGGATGCCAATGGGTCTCGCGGCTCATGTATACCACCACTCTACACCA	1621
QY	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
DB	1622	CTCCCTCTGGGGGCCCTCCAGAGGGGTGGAGTCTGTACACAGCTTACCATGTGCTACT	1681
QY	593	ysHisLeuGluProValArgCysGlnAlaProProArgCysProSerGluAlaSerG	613
DB	1682	GCCACTTGGAGCCAGTCCGTGGCAGGACACCCCTCCAGATGCCATCGAGGCACTG	1741
QY	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI	633
DB	1742	GTAGGACTGTGGGTAGTGGGAAGGTGTACCCACTGTGCATACCAGGCCCTCCACCA	1801
QY	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS	653
DB	1802	TACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGGCCCCCACCCTCA	1861
QY	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
DB	1862	GCTTCAACATCCCACTGGGCCCTTCAGCTCCATGCACAAAGCTCTCGAGACACAGAT	1921
QY	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
DB	1922	CGGAGCCTGCATAGCTCTCGCAAAATCTCCAGCCCTTGTCCAAAGGCACAGTGGAG	1981
QY	693	laCysGlyProAspSerCysAlaArgThrGlyAlaGlyGluProGluSerA	713
DB	1982	CCTCGCGGGCCGAGTGTCCCTACTGTGCCGAGCAGGAGCAGGAGCCAGTCCG	2041
QY	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
DB	2042	CTGACCATGTCTATGCCCTGACTCAGACAGCGAGGCTGTGTATAGTTCCACACAGAC	2101
QY	733	lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA	753
DB	2102	AGCACGTGACCTCCGGATCCCCACAGCCGGGGCCGACAGCGAGCCTGGGGCCAGATG	2161
QY	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
DB	2162	CAGAGCCTAGTCTGTCTGTCTTCTGGAGGCTGATCTGTGACACATTCGGAAGATCG	2221
QY	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
DB	2222	TAGTAGCAATATCTTTGGCGGGGAATCATGATCGCCATCTCTGTCATACACTCAGCA	2281
QY	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
DB	2282	TGGSCATCGAGTACCACAGCAGCCCGAGGAGCTCACCAGCCCTGGAATCAGCAACA	2341
QY	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProp	833
DB	2342	TCGTCTTCCACAGCCTCTCGCCTTGGAGATGTGCTGTAACCTGTCTGTCTAGCGTCC	2401
QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT	853
DB	2402	TTGGCTACATTAAGAATCCCTTACAAATCTTTGATGGTGTCTGTGGTTCATCAGTGTG	2461
QY	853	rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
DB	2462	GGGAGATTGTGGGCCACAGGAGGTGGCTGTCTGGTGTCTGGACCTTCGGCTGTATGC	2521
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
DB	2522	GGGTGCTGAAGCTGTGTGCTTCTGCGGCCCTTGACGCCAGCCAGCTCGTGTGCTCATGA	2581

QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
DB	2582	AGACCATGGACACAGTGGCCACCTTCTGCAATGCTCTCTCATGCTGTTTCATCTTCA	2641
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
DB	2642	GCATCTCTGGGCATGCATCTCTTTGGTTGCAAGTTGCGCATCTGAACGGGATGGGAC	2701
QY	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
DB	2702	TGGCAGACCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCA	2761
QY	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
DB	2762	TGACTCAGGAAGACTGGAATAAAGTCTCTTACAAAGCATGGCCCTCCACATCGTCTT	2821
QY	973	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993
DB	2822	CTGCTCTTTACTTCTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTTAACT	2881
QY	993	alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerClup	1013
DB	2882	TGGCCATCTTGTGGGAAGATTCAGGCAGAGGAGATGCCCAAGTCTGTAGTCAGAGC	2941
QY	1013	roAspPhePheSerProSerValAspGlyAspGlyArgLysLysLysArgLeuAlaLeuV	1033
DB	2942	CTGATTTCTTTTCGCCAGTGTGGATGGGTGATGGGACACAAAGAGCGCTTGGCCCT	3001
QY	1033	alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT	1053
DB	3002	TGGCTTTGGGAGAACACCGCGAACTACGAAAGAGCCTTTTGGCCACCCCTCATCATC	3061
QY	1053	hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyAlaAlaLeuG	1073
DB	3062	CGCTCGCACACCAATGTACACCCCAAGAGCTCCAGCAGGTGTGGGGAGACACTGG	3121
QY	1073	lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyValAlaAlaHisG	1093
DB	3122	GCTCTGGCTCTCGACGTACCACTAGCAGTGGGTCCGCTGAGCTGGAGCTGCCACCAT	3181
QY	1093	luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS	1113
DB	3182	AGATGAAATGTCCGCCAAGTGCCTCCGAGCTCCCGCACAGTCTGAGTCGCGCAAGCA	3241
QY	1113	erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA	1133
DB	3242	GCTGGACACAGCAGCGCTCCAGCAGAAACAGCTGGGCGCGGCCCCCAGCTTAAAGCG	3301
QY	1133	rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG	1153
DB	3302	GGAGCCGAGCGGGGAGCGGAGGTCTCTGTCTGTGGAGAGGGCCAGGAGTCAAGATG	3361
QY	1153	luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
DB	3362	AGCAGGAAAGTTCAGAAGAGACCGGGCCAGCCAGCAGCAGTGCACCATCGCCACAGG	3421
QY	1173	lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG	1193
DB	3422	GTTCTTGGAACTGAGGCCAAGATTCCTTTGACCTGCTGACACTCTCAGGTGCGCGG	3481
QY	1193	lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL	1213
DB	3482	GGCTGCACCGCACAGCCGCGCGGAGCTCTGCTCTGAGCACCAGACTGTAAATGGCA	3541
QY	1213	ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA	1233
DB	3542	AGTCGGCTTCAGGCGCTTGGCCCGCACCTCGAGGACTGATGACCCCACTGGATGGGG	3601
QY	1233	spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS	1253
DB	3602	ATGATGACAAATGATGAGGGAATCTGAGCAAAAGGGGAACGATACAAAGCTGGGTCA	3661
QY	1253	erArgLeuProAlaCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG	1273

Db	3662		CCCCGCTTCTCCCTGCTGTCGCCAGGAGGAGATTCCTGGTCGGCCTATATCTTCTCTCTC	3721	Db	4742	TCCTGTGCCACCACTGTGTATACAGCCACTACTCTGACCTCTTCATCACTGGTGTCTATCG	4801
Qy	1273		lnSerArgPheArgLeuLeuCysHisArgIleThrHisIysMetPheAspHisValV	1293	Qy	1622	lyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluA	1642
Db	3722		AGTCAAGGTTTCGTCTCTCTGTCACCGGATCATCACCCACCAAGATGTTGACCATGG	3781	Db	4802	GGCTGAAGCTGGTCACTATGGCCATGAAACATTTACAGCAGCCAGATCTCTGGACGAGG	4861
Qy	1293		allLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProIysIleAspP	1313	Qy	1642	lalLeuIysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheIysL	1662
Db	3782		TCCTCGTCTATCATCTTCCTCAACTGTATCACCATCGTATGGAGGCCCAAAATTGACC	3841	Db	4862	CTCTGAAGATCTGCAATATCATCTTTACCGTCACTCTTTGTCTTTGAGTCAGTTTTCANAC	4921
Qy	1313		roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL	1333	Qy	1662	euValAlaPheAlaPheArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaI	1682
Db	3842		CCACAGCGCTGAGCGCATCTTCTGACCTCTCCAACTTACATCTTCACGGCAGTCTTTC	3901	Db	4922	TTGTGGCTTTGGCTTCCGCGTTTCTTCAGACAGGTGGAAACAGCTGGACCTGGCTA	4981
Qy	1333		euAlaGluMetThrValIysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrL	1353	Qy	1682	leValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuP	1702
Db	3902		TAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGCTTGGGGAGCAGGCTTACC	3961	Db	4982	TTGTGCTTCTGCTCCATCATGGGCATCACCTGAGGAGATTTAGGTCATCTGTCTGCTGC	5041
Qy	1353		euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL	1373	Qy	1702	rolleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAraValLeuIysL	1722
Db	3962		TGGCGACAGCTGGATGTGCTGGACGGCTTGTGTGCTCATCTCCGTCACTCGCATCC	4021	Db	5042	CCATCAACCCACCATCATCCGTATCATGAGGTGCTCCGATTTGCTCGAGTTCTGAAGC	5101
Qy	1373		euValSerMetValSerAspSerGlyThrIysIleLeuGlyMetLeuArgValLeuArgL	1393	Qy	1722	euLeuIysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProG	1742
Db	4022		TGGTCTCATGTTCTCCGACAGCGGACCAAGATCCTTGGCATGCTGAGGGTGTGCGGC	4081	Db	5102	TGTTGAAGATGGCTGTGGGATGTCGGGCACCTGCTGCACACGGTGATGCAGGCCCTGCCCC	5161
Qy	1393		euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIysLeuValV	1413	Qy	1742	lnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyV	1762
Db	4082		TGCTGGGACCCCTGCGTCCACTCAGGTGTCATGACCGCGGCCAGGACTGAGCTGTGG	4141	Db	5162	AGGTGGGGAAACCTGGGACTTCTTTCATGTTATTTGTTTTCATCTTTGCAGCTCTGGCGG	5221
Qy	1413		alGluThrLeuMetSerSerLeuIysProIleGlyAsnIleValIleCysCysAlaP	1433	Qy	1762	alGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgH	1782
Db	4142		TAGAGACTCTGATGTCATCCCTCAACCCATTCGCAACATTTGGTCACTTGTGTGGCT	4201	Db	5222	TGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGGGTGCGC	5281
Qy	1433		hePheIleIlePheGlyIleLeuGlyValGlnLeuPheIysGlyPhePheValCysG	1453	Qy	1802	isAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyA	1802
Db	4202		TCTTCATCATTTTGGAAATCTCGGGGTGACGCTCTTCAAGAGGAAGTCTTCTGCTGTC	4261	Db	5282	ATGCCACCTTTAGGAACTTTGGTATGGCTTTTTCAGACCTCTTCGAGTCTCCAGTGGT	5341
Qy	1453		lnGlyGluAspThrArgAsnIleThrAsnIysSerAspCysAlaGluAlaSerTyrArgT	1473	Qy	1802	spAsnTrpAsnGlyIleMetIysAspProSerArgAspCysAspGlnGluSerThrCysT	1822
Db	4262		AGGTGAGGACACACAGGACATCACTAACAAATCCGACTCGCTGAGGCCAGCTACCGAT	4321	Db	5342	ACNACTGGANATGTTATTTATGAGGACACCTCCGAGACTGTGACGAGGTCCACTGCT	5401
Qy	1473		rpValArgHisIysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValI	1493	Qy	1842	yrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValL	1842
Db	4322		GGGTCCGGCAACAAGTACAACTTTCACAACTGGGCCAGGCTCTGATGCTCTGTTGTGC	4381	Db	5402	ACAACACTGTCACTCTCCCTATCTACTTGTGTCTCTGCTGACGGCCCACTGTTGTGC	5461
Qy	1493		euAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValA	1513	Qy	1842	euValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnIysGluAlaL	1862
Db	4382		TGGCTCCNAGATGGTTGGTTGACATCATGATGATGGCTGGATGCTGTGGGTGTGG	4441	Db	5462	TGGTCAACGTGTCTATAGCTGTGCTGATGAGCACCTCGAGAAAGCAACAAAGAGGCCA	5521
Qy	1513		spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL	1533	Qy	1862	ysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnP	1882
Db	4442		ATCAGCAGCCCATCATGAACACACACACCTCGATGCTGCTATCTCTCTCTCTCTCC	4501	Db	5522	AGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGTGAAGACGCTCAAGCCCGCAGC	5581
Qy	1533		euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL	1553	Qy	1902	roHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrA	1902
Db	4502		TCATCGTGGCTCTCTTGTCTGAAACATGTTGTGGGCGTGGTGGAGNACTTCCATA	4561	Db	5582	CCCACTCCCGCTGGGACGCCCTTCTCTGCCCCGGGTGGAGGGTGTCAACAGTACTG	5641
Qy	1553		ysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluIysArgLeuArgA	1573	Qy	1902	spSerProIysProGlyAlaProHisThrAlaHisIleGlyAlaAlaSerGlyPheS	1922
Db	4562		AGTCAGACAGACACAGGAGGAGGAGGAGCGCGCGTGTGAGAGAAGCGACTACGGA	4621	Db	5642	ACAGCCCTTAAGCTGGGGCTCCACACCACTGCCACATTTGGAGCAGCTCGGGCTCT	5701
Qy	1573		tgLeuGluIysIysArgArg-----SerIysG	1582	Qy	1922	erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA	1942
Db	4622		GGCTGGAGAAAAAGAGAGAAATCAATGTTGGACGATGTAATGCTCCCGGAGCTCAG	4681	Db	5702	CCCTTGAGCAGCCACGATGGTACCCCGGAGGAGGTGCCAGTCTCTGCCCAATGACAGCT	5761
Qy	1582		luIysGlnMetAlaGluAlaGlnCysIysProTyrTyrSerAspTyrSerArgPheArgL	1602	Qy	1942	spLeuLeuThrValArgIysSerGlyValSerArgThrHisSerLeuProAsnAspSerT	1962
Db	4682		CCAGCGCTCGTCAGAGCCCACTGCAAGCCCTACTACTCTGACTACTCTGAGATTCGGC	4741	Db	5762	ACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGAGCGCACTCTCTGCCCAATGACAGCT	5821
Qy	1602		euLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleG	1622	Qy	1962	yrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuP	1982
					Qy	5822	ACATGTGCCCAATGGAGGACCTGCTGAGAGATCCCTTAGGACACAGGGGCTGGGGCTCC	5881

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Qy 1982 roLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI 2002
Db 5882 CCAAGGCCAGTCCAGGCTCCATCTGTCCGTTCTACTCCCAACAGCAGACACACAGCTGCA 5941
Qy 2002 leLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpG 2022
Db 5942 TCCTACAGCTTCCCAAGAGTGCACATCTATCTGCTCCAGCCTCATGGGGCTCCCACTGGG 6001
Qy 2022 lyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgA 2042
Db 6002 GCGCATCTCCCTAAACTACCCCACTCCGCGCTCCCTCTGCTGCTGCTGCTGCTGCTGCTG 6061
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Qy 2082 lySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerIleHisIleA 2102
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Qy 2182 erCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyG 2202
Db 6482 GCTGCTGGACAGCGGCTCCCAACCCGCTATGTCCAAGCCCTCAAGCCTCGGGGGCC 6541
Qy 2202 lnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerI 2222
Db 6542 AACCTCTTGGGGGTCCTGGGAGCGCGCTAAGAAAAAAGTCAAGCCCACTATCTCTA 6601
Qy 2222 leAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgA 2242
Db 6602 TAGACCCCGCGAGAGCAGCGGCTCTCGGCCCCCATGCACTCTGCTGCTGCTGCTGCTGCTG 6661
Qy 2242 rgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrA 2262
Db 6662 GGAGGGCGCGCGCGCAGTGACTCTAAGATCCCTCGGTCTCCAGCCCTCCAGCAGCAGG 6721
Qy 2262 laAlaSerProSerProLysIleAspThrLeuSerLeuSerGlyLeuSerSerAspProT 2282
Db 6722 CTGCCTCACCTTCCCAAGAAAGACACGCTGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 6781
Qy 2282 hrAspMetAspPro 2286
Db 6782 CAGACATGGACCCC 6795
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RESULT 7

ID AAX83488

XX AAX83488 standard; cDNA; 6741 BP.

AC AAX83488;

XX 07-DEC-1999 (first entry)

XX

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DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavTld) cDNA.
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX Rattus sp.
XX WO9929847-A1.
XX 17-JUN-1999.
XX 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO ) UNIV LOYOLA CHICAGO.
XX Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.
XX P-PSDB; AAY14593.
XX New T-type voltage-gated calcium channels.
XX Disclosure; Page 94-103; 138pp; English.
XX This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCavTld. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX SQ Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.: 0 Length: 6741
Score: 11747.50 Matches: 2242
Percent Similarity: 99.47% Conservative: 1
Best Local Similarity: 99.42% Mismatches: 3
Query Match: 97.67% Indels: 9
DB: 2 Gaps: 1
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US-09-611-257A-24 (1-2287) x AAX83488 (1-6741)

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Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGGATGGAGCGGGCGCGGAGGAGTGGGAGCGCCCGTACGCTTCACGC 61
Qy 54 SerSerThrThrCysProGlyProGlyVala-AlaGlyVala-GlySerThrGluLysAspP 73
Db 62 AGCTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGCGGGGTTCACGGGAAGGACC 121
Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCGGTACCCGGGGCTAGCCCGCGTGTGTTT 181
Qy 93 hepheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTTGAGCCAGGACAGCGCCCGCGGAGCTGGTGTCTCCCGCACGGTCTGTAAACC 241
Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAenCysValThrLeuGlyMetP 133
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Db	242		CGTGGTTCCAGCGAGTCAGTATGCTGGTCAATCTCTCAACTGTGTGACTCTGGGTATGT	301
QY	133		heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleIleuGlnAlaPheA	153
Db	302		TCAGGCGGTGTGAGGACATGCTGTGTGATCCACGCGTCCGGATCTCGAGGCTTCG	361
QY	153		spAspPheIlePheAlaPheAlaValGluMetValVallysMetValAlaLeuGlyI	173
Db	362		ATGACTTCATCTTGTGCTTCTTGTGTGGAATGGTGTGAAGATGGTGGCTTGGGCA	421
QY	173		lePheGlyLysIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI	193
Db	422		TCCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTCATTGTCA	481
QY	193		leAlaGlyMetLeuGlyTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT	213
Db	482		TTGCAGGGATGCTGGAGTATTCCTGGACCTGCAGAACGTCAAGTCTCTCCGAGTCAGGA	541
QY	213		hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
Db	542		CAGTCCGTGTGCTGGACCGCTCAGGGCCATTAAACCGGTGGCCAGCATGCGCAATCTCG	601
QY	233		alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheV	253
Db	602		TCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGTGCTCTGTCTTCG	661
QY	253		alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
Db	662		TCCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGAGGACTGCTTCGCAACCGGT	721
QY	273		ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722		GCTTCTCCCGAGAACTTCAGCTCCCTGAGCGTGGACCTGGAGCCCTATTATACAGA	781
QY	293		hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782		CAGAGAAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCTCTGGGAGAAATGGCATGAT	841
QY	313		erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA	333
Db	842		CCTGCAGAGGTGTGCCACACACTGCTGGGGAAGCGGTGGTGGCCACCTTCGAGTCTGG	901
QY	333		spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
Db	902		ACTATGAGACCTATAAACAGTTCAGAACACCCACTGTGTCACTTGGAAACAGTACTATA	961
QY	353		hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValaIleAsnPheAspAsnIleG	373
Db	962		CCAACTGCTCTCGGGGCGAGCAACACCTTCCTCAAGGGCGCCATCAACTTTGACAACTTG	1021
QY	373		lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPheValAspIleMetT	393
Db	1022		GCTATGCTGGATCGCCATCTTCCAGGTCAATCACACTGGAGGCTGGGTCCACATCATGT	1081
QY	393		yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV	413
Db	1082		ACTTCGTAAATGAGCGTCACTCTCTTCAACCTTCACTTACTTCTTCTCATCATCG	1141
QY	413		alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT	433
Db	1142		TGGGCTCTCTTTCATGATCAACCTGTGCTGGTGTGATTGCCACGAGTCTCCGAGA	1201
QY	433		hrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS	453
Db	1202		CCAAACAGGGGAGAGTCACTGATGCGGAGCAGCGGTGATGATTCCTGTCCATATGTA	1261
QY	453		erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV	473
Db	1262		GCACCTTGGCAAGCTTCTCTGAGCCAGGAGCTGTCTATCAGGAGCTACTCAAGTACCTGG	1321
QY	473		alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVala	493
Db	1322		TGTACATCTCCGAAAGCAGCCGGAAGGTGGCCAGGTCTCTAGGGCTATAGGCGTGC	1381
QY	493		rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys	513
Db	1382		GGGCTGGCTGTCTCAGCAGCCAGTGGCCGTAGTGGGAGGAGCCACAGCCAGTGGCA	1441
QY	513		erCysThrArgSerHisArgArgLeuSerValHisLeuValHisHisHisHisH	533
Db	1442		GCTGCATCTCCTCACACCGTCTGTCTGTCTCCACACCTGGTCCACCATCATCACACC	1501
QY	533		ishHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502		ACCATCACCACTACCACTGGGTAAATGGGACGCTCAGAGTTCCCGGGCCAGCCAGAGA	1561
QY	553		leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT	573
Db	1562		TCCAGGACAGGGATGCAATGGGTCTCGCCGGTCTATGCTTACCAACCACTCTTACACCCA	1621
QY	573		hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
Db	1622		CTCCTCTGGGGGCGCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTACCATGCTGACT	1681
QY	593		ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
Db	1682		GCCACTTGGAGCCAGTCCGTTGCCAGGACCCCTCCAGATGCCATCGGAGGCACTGTG	1741
QY	613		lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI	633
Db	1742		GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCTCTCCACAGAGA	1801
QY	633		leLeuLysAspLysAlaLeuValGluValAlaProProProGlyProProThrLeuThrS	653
Db	1802		TACTCAAGGATAAAGCACTAGTGGAGGTGGCCCGCCAGCCCTGGGGCCCCCCCCCTCACCA	1861
QY	653		erPheAsnIleProProGlyProPhePheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
Db	1862		GCTTCAAAATCCCACTGGGCGCTTCAGCTCCATGCACAAGCTCTCTGGAGACACAGATA	1921
QY	673		hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922		CGGGAGCTGCCATAGTCTCTGCAAAATCTCCAGCCCTTGTCTCAAGGACAGTGGAG	1981
QY	693		laCysGlyProAspSerCysProTyrCysAlaArgThrGlyValaGlyGluProGluSerA	713
Db	1982		CCTGGCGGCGGACAGTGTCTCTACTGTGCCCGGACAGGAGCAGGAGCCAGAGTCCG	2041
QY	713		laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
Db	2042		CTGACCATGTCTGCTGACTCAGACAGCGGCTGTGTATGATGTTTCAACAGGACGCTC	2101
QY	733		lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA	753
Db	2102		AGCACAGTCACTCCGGATCCCAAGCGGCGGACAGCGGAGCCCTGGGCCCGAGATG	2161
QY	753		laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
Db	2162		CAGAGCTAGTCTGTGCTGGCTTCTGGAGGCTGATCTGTGACACATTCGGAAGATCG	2221
QY	773		alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
Db	2222		TAGATAGCAAAATCTTTGGCGGGGAATCATGATCGCCATCTCTGGTCAATATACACTCAGCA	2281
QY	793		etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2282		TGGGCATTCGAGTACCCAGCAGCCCGGAGGCTCACCAAGCCCTGGAAATCAGCAACA	2341
QY	813		leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProp	833
Db	2342		TCGTCTTCCACAGCCTCTTCCGCTTGGAGATGTGTGTGAACCTGTGTCTAGCGTCCCT	2401
QY	833		heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT	853
Db	2402		TTGGCTCATTTAAGATCCCTTACAACTCTTTGATGGTGTCTATGTTGTCTCATGTGTGT	2461

853 rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
2462 GGGAGATTGTGGGCCACAGGAGGTGGCTGTGGTGTGGGACCTTCGGCTGATGC 2521
873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnA:ggInLeuValLeuMetL 893
2522 GGGTGTCTGAAGCTGGTGGCTTCCTGGCGGCCCTGCAGCGCAGCTCGTGTGCTCATGA 2581
893 ysrThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheHis 913
2582 AGACCATGGACAAGCTGGCCACCTTCCTGCATGCTCCTCATCTTCACTTCATCTCA 2641
913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
2642 GCATCCTGGGCATGCTCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACGT 2701
933 euProAspArgLysAsnPhaAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
2702 TGGCAGACCGGAAGATTTCCGACTCCCTGTCTGGGCCATCGTCACTGTCTTTCCAGATT 2761
953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
2762 TGACTCAGGAAGACTGGAATAAAGTCTCTACACGGCATGGCCCTCCACATCGCTTTGGG 2821
973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
2822 CTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTCTCTTTAACTGTGTG 2881
993 alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
2882 TGGCCATTCTTGTGGAAGGATTCAGGAGGAGATGCCACCAAGTCTGAGTCAGAGC 2941
1013 roAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV 1033
2942 CTGATTTCTTTTGGCCAGTGTGGATGGTATGGGACAGAAAGCGCTTGGCCCTGG 3001
1033 alAlaLeuGlyGluHiAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisT 1053
3002 TGGCTTTGGGAGAACACCGGNACTACGAAAGACCTTTTGGCCACCTCTCATCATCATA 3061
1053 hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG 1073
3062 CGGCTGGCAGACCAATGTCAACCCCAAGAGTCCAGCAGAGGTGTGGGGAGACACTGG 3121
1073 lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisG 1093
3122 GCTCTGGCTCTCGACGTACAGTAGCAGTGGTCCGCTGAGCCTGGAGCTGCCACCATG 3181
1093 luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
3182 AGATGAATGTCCGCCAAGTGGCCGAGCTCCCGCAGCTCCCTCGAGTGGGCAAGCA 3241
1113 erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
3242 GCTGGACAGCAGCGCTCCAGCAGGAACAGCTGGCGGCCGCCGCCCTAAAGCGGA 3301
1133 rgSerProSerGlyGluArgArgSerLeuSerGlyGlyGlnGluSerClnAspG 1153
3302 GGAGCCCGAGCGGGAGCGAGGTCCCTGTCTGGAGAGGGCGAGGAGTCCAGGATG 3361
1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
3362 AGGAGGAAGTTTCAGAGAGAGACCGGCCAGCCAGCAGGAGTACATCGCCACAGGG 3421
1173 lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
3422 GTTCTTTGGAACGTGAGGCCAAGATTCTTTGACCTGGCCTGACACTCTGCAGGTGCCGG 3481
1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
3482 GGCTGCACCGCACAGCCGCGGAGCTCTGCTCTGAGCACCAGACTGTAAATGGCA 3541

1213 ysrSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
3542 AGTCGGCTTCAGGGCGTTTGGCCGACACCTTGAGGACTGATGACCCCAACTGGATGGG 3601
1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
3602 ATGATGACAAATGATGAGGGAATCTGTGCAAGGGAACGCATACAAGCCCTGGGTGCAT 3661
1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
3662 CCGGCTTCTGCTGCTGTTCGAGAGCGAGATTCTCGTGGCTATATCTTTCTCTCTC 3721
1273 lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
3722 AGTCAAGTTTCTGCTCTCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTG 3781
1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313
3782 TGCTCGTCACTCATCTTCTCAACTGTATCACTCGCTATGGAGCGCCCAAAATTGACC 3841
1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
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1333 euAlaGluMetThrValLysValAlaAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrL 1353
3902 TAGCTGAAATGACAGTGAAGTGGTGGCACTGGGCTGGTGTCTTTGGGAGCAGGCCATCC 3961
1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
3962 TGGCAGCAGCTGGAATGTCTGAGCGCTTGTGTGGTGTCTCATCTCGCTCATCGACATCC 4021
1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
4022 TGGTCTCCATGGTCTCCGACAGCGCACCAAGATCTTGGCATCTCTGAGGCTGCTCGGC 4081
1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
4082 TGCTGGGACCTTCGCTCCACTCAGGGTCACTCAGCGGGCCCCAGGGACTGAAGCTGGTGG 4141
1413 alGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaP 1433
4142 TAGAGACTCTGTATGTCTATCCCTCAAAACCCATGCGCAACATTTGTGTGTGTGCT 4201
1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
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1473 rpValArgHisLysTyrAsnPhaAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
4322 GGGTCCGGCAACAAGTCAACTTTGACAACTGGGCCAGGCTCTGATGTCTCTGTGTGTGC 4381
1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
4382 TGGCTTCAAAGGATGGTGGGTGACATCATGATGATGGCTGGATGCTGTGGGTGTGG 4441
1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
4442 ATCAGCAGCCCATCATGAACCAACCAACCCCTGGATGCTGTATCTTCTCTCTCTCTCC 4501
1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValValGluAsnPheHisL 1553
4502 TCATCGTGGCTTCTTTGTCTCTGAACATGTTTGTGGCGCTGGTGTGGAGAACTTCCATA 4561
1553 ysrCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
4562 AGTCAGACAGCACCAAGGAGGAGGAGGAGCGGCGGCTGAGGAGAGGAGCTACGGA 4621
1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProT 1593

Db	4622	GCTGGAGAAAAGAGAGG-----AAAGCCAGTGCAAGCCCT	4660	Db	5681	AGAGGTGCGAGTCCCTTAGGACAGAGCTGCTGAGTGTGAGAAAGTCTGTGTGTCAGCC	5740
Qy	1593	YrTySerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL	1613	Qy	1953	rgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS	1973
Db	4661	ACTACTCTGACTACTCGAGATTCCGGCTCTTGTGCCACACCTGTGTACCGACCACTACC	4720	Db	5741	GGACGCACTCTCTGCCCAATACAGCTACATGTGTGCCCAATGGGAGCACTGTCTGAGAT	5800
Qy	1613	euAspLeuPheThrThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT	1633	Qy	1973	erLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH	1993
Db	4721	TGACCTCTTCATCATCTGTGTGTCATCGGGCTGAACTGTGTCTACTATGGCCATGGACATT	4780	Db	5801	CCCTAGGACACAGGGCTGGGGCTCCCCAAAGCCAGTCAGGCTCCATCTTCTCGGTTT	5860
Qy	1633	YrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI	1653	Qy	1993	isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL	2013
Db	4781	ACCAGAGCCCAAGATCCTGGAGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCA	4840	Db	5861	ACTCCCAACAGCAGACACAGCTGCATCTACAGCTTCCCAAGATGTGCATATCTGC	5920
Qy	1653	lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlnA	1673	Qy	2013	euGlnProHisGlyAlaProThrThrGlyValIleProLysLeuProProGlyArgS	2033
Db	4841	TCCTTGTCTTTGAGTCAGTTTCAAACTTGTGGCCCTTTCGGTTCGCCCTTCTTCCAGG	4900	Db	5921	TCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCCTAAACTACCCCACTGGCCGCT	5980
Qy	1673	spArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG	1693	Qy	2033	erProLeuAlaGlnArgProLeuArgGlnAlaIleAlaIleArgThrAspSerLeuAspV	2053
Db	4901	ACAGGTGGAACAGCTGGACTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGG	4960	Db	5981	CCCTCTGGCTCAGAGGCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATG	6040
Qy	1693	luGluIleGluValAsnLeuSerLeuPheLeuProThrIleIleArgIleMetArgV	1713	Qy	2053	alGlnGlyLeuGlySerArgGluAspLeuSerGluValSerGlyProSerCysProL	2073
Db	4961	AGGAGATTGAGTCAATCTCTGCTGCCCATCAACCCCACTATCCGTATCATGAGGG	5020	Db	6041	TGCAGGGCTCTGGGTAGCGGGAAGACCTGTGTGTGAGAGGTGAGTGGGCCCTCTCTGCCCTC	6100
Qy	1713	allLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL	1733	Qy	2073	euThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI	2093
Db	5021	TGCTCCGCAATTGCTCGAGTTCTGAGCTGTGAGATGGCTGTGGGCTGTGGGCACTGC	5080	Db	6101	TGACCCGGTCTCTATCTCTTCTGGGGGGGTGCCAGCCCTTGGCCAGGCTTGGAACCCA	6160
Qy	1733	euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL	1753	Qy	2093	leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS	2113
Db	5081	TGCACAGGTGATGACAGGCTTGGGTGGGCTGGGCACTTGGGACTTCTCTCATGTAT	5140	Db	6161	TCCAGAGCAAAAGTCTCCAAAGCACATCCGCTGCCAGCCCTTGGCCAGGCTTGGAACCTGA	6220
Qy	1753	euPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT	1773	Qy	2113	erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT	2133
Db	5141	TGTTTTTTCATCTTTCAGCTCTGGGCTGGGCTGGGCTTTGGAGACCTTGGAGTGTGATGAGA	5200	Db	6221	GCTGGGCAAGGACCTCCAGAGCACAGACAGCAGCTTAGAGCTGGACAGGAGCTGAGCT	6280
Qy	1773	hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL	1793	Qy	2133	rpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL	2153
Db	5201	CACACCTTGTGAGGGCTTGGGTGGGCTGGGCTTGGGCACTTTAGGAACCTTTGGTGTG	5260	Db	6281	GGATTTCAGGACACTCTCTTCCAGCAGCAGGAAAGAACCTCTGTTCACAGGGACCTGA	6340
Qy	1793	euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA	1813	Qy	2153	ysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspG	2173
Db	5261	TGACCCCTCTCCGAGTCTCCACTGGTGCAACTGGAATGGTATTATGAGACACCCCTCC	5320	Db	6341	AGAAGTGTCTACAGTGTAGAGACCCAGAGCTGAGCGGCGAGGCTGGGTCTGGCTAGATG	6400
Qy	1813	rgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS	1833	Qy	2173	luGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuL	2193
Db	5321	GGAGTGTGACAGGAGTCCACTGCTACACACTGTCTATCTCCCTTATCTTCTGTGT	5380	Db	6401	AAACAGCGGAGACACTCCATTGTCTGTCAGCTGTCTGACAGCGGCTCCCAACCCCGCTAT	6460
Qy	1833	erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH	1853	Qy	2193	ysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysL	2213
Db	5381	CCCTTCTGTGACGGCCCAAGTTGTGTGGTCAACGTGGTCAAGCTGTGTGTGATGAAGC	5440	Db	6461	GTCCAAAGCCCTCAAGCCTCGGGGGCAACCTCTTTGGGGGTCTCTGGAGCCCGGCTTAAGA	6520
Qy	1853	isLeuGluLysSerAsnLysGluAlaLysGluAlaGluLeuGluAlaGluLeuGluL	1873	Qy	2213	ysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProP	2233
Db	5441	ACCTGGAAGAAAGCAACAAAGAGCCAGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGC	5500	Db	6521	AAAACTCAGCCCAACCCAGTATCTCTATAGACCCCGGAGAGCCAGGCTCTCGGCCCC	6580
Qy	1873	euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpP	1893	Qy	2233	roCysSerProGlyValCysLeuArgArgAlaPheAlaSerProLysSerLysAspProS	2253
Db	5501	TGGAGATGAAGAGCTCAGCCCGCAGCCCACTCCCGCTGGGCAAGCCCTTCTCTGGC	5560	Db	6581	CATGCACTCTCGTGTCTGCTCAGGAGGAGGGCGCGGCGGCTGACTCTTAAGGATCCCT	6640
Qy	1893	roGlyValGluGlyValAsnSerThrAspSerProLysProGlyValAlaProHisThrA	1913	Qy	2253	erValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuS	2273
Db	5561	CCGGGTGGAGGGTGTCAACAGTACTGACAGCCCTTAGCCTGGGCTCCACACCACTG	5620	Db	6641	CGGTCTCAGCCCTTTCAGACGACCGGTGCTCTACCCCTCCCAAGAAAGACACGCTGA	6700
Qy	1913	lahisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG	1933	Qy	2273	erLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286	
Db	5621	CCACACATTGGAGCAGCTCTGGGCTTCTCCCTTGGAGCACCCACGATGGTACCCACCCG	5680	Db	6701	GTCTCTCTGTGTGTCTTCTTGTGACCAACAGACATGGACCCC 6741	
Qy	1933	luGluValProValProLeuGlyProAspLeuThrValArgLysSerGlyValSerA	1953				

RESULT: 8
AAD04756
ID AAD04756 standard; cDNA; 7741 BP.

XX AC AAD04756;
 XX DT 17-JUL-2001 (first entry)
 XX DE Human T-type low voltage activated calcium channel alpha1G-c cDNA.
 XX KW Human T-type low voltage activated calcium channel alpha1G-c; stress;
 KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
 KW endocrine disorder; respiratory disorder; peripheral muscle disorder;
 KW muscle excitability; fertilisation; contraception; hypertension;
 KW neuronal firing regulation; cardiovascular disorder; gene therapy;
 KW forensic analysis; epidemiological study; neuroleptic; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT 5'UTR 1. 522
 FT CDS /*tag= a
 FT 523..7344
 FT /*tag= b
 FT /product= "Human T-type low voltage activated calcium
 FT channel alpha1G-c protein"
 FT /transl_except= (pos:3934..3936, aa:Gln)
 FT /transl_except= (pos:3946..3948, aa:Gln)
 FT /transl_except= (pos:5560..5562, aa:Pro)
 FT /transl_except= (pos:5569..5571, aa:Gln)
 FT /note= "The CDS is specifically claimed in claim 2 as SEQ
 FT ID NO:3"
 FT 3'UTR 7345..7741
 FT /*tag= c
 XX WO200130844-A1.
 XX 03-MAY-2001.
 XX 06-OCT-2000; 2000WO-US027761.
 XX 26-OCT-1999; 99US-00426998.
 XX (ORTH) ORTHO-MCNEIL PHARM INC.
 XX Dublin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
 XX WPI: 2001-300486/31.
 XX P-PSDB; AAE01019.
 XX New nucleic acid encoding human calcium channel protein, useful for
 XX identifying specific modulators and potential pharmaceuticals for
 XX treating e.g. epilepsy.
 XX Claim 2; Page 76-81; 115pp; English.
 XX The invention relates to isoform of human T-type low voltage activated
 XX calcium channel (alpha1G-c) cDNA and protein. Cells transformed with
 XX calcium channel DNA to express calcium alpha1G-c channel protein are used
 XX to identify specific modulators (antagonists or agonists). These
 XX modulators are useful as therapeutic agents and are used for treating
 XX wide range of calcium alpha1G-c channel-mediated disorders, e.g. stress
 XX epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
 XX endocrine disorders, respiratory disorder, peripheral muscle disorder,
 XX muscle excitability, fertilisation, contraception, disorders involving
 XX hypertension, neuronal firing regulation, potentiation of synaptic
 XX signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
 XX hyperthyroidism, angina pectoris). Calcium alpha1G-c channel DNA is useful
 XX for isolating and identifying related molecule mutations. It is also
 XX optionally used as antisense sequences, in gene therapy. Calcium channel
 XX alpha1G-c DNA, protein and antibodies are useful for forensic analysis,
 XX diagnosis and epidemiological studies, by standard hybridisation or
 XX immunological assays. The present sequence is T-type low voltage
 XX activated calcium channel alpha1G-c cDNA. This sequence is isolated from
 XX human thalamus cDNA library

SQ Sequence 7741 BP; 1469 A; 2496 C; 2287 G; 1489 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0 Length: 7741
 Score: 11066.50 Matches: 2134
 Percent Similarity: 93.81% Conservative: 33
 Best Local Similarity: 92.38% Mismatches: 112
 Query Match: 92.01% Indels: 31
 DB: 4 Gaps: 5
 US-09-611-257a-24 (1-2287) x AAD04756 (1-7741)
 Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
 Db 431 CGCGGGGGCCCCCGGGTTCGGTGAGGACACCTCTCTGAGGGGGCGCGCTTCCCTCT 490
 Qy 23 SerAspProGlyProArgLeuAlaArgGlyTTPThrArgArgMetGluArgAla 42
 Db 491 CGGATCGCCCGGGGGCCCCGGCTGGCCAGAGGATGGACGAGGAGGATGAGCGGGCG 550
 Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
 Db 551 CCAGAGAGTCCGGACAGCCCGGAGCTTCATGGGGCTCAACGACCTCTCGGGGGCCGGGG 610
 Qy 63 Ala-AlaGlyAla-GlySerThrGlyLysAspProGlySerAlaAspSerGluAlaGluG 82
 Db 611 GCAGGGCGGGGGCGGGGTTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670
 Qy 82 LysLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
 Db 671 GGCTGGCGTACCCCGGGCGCTGGCCCGGTGGTTCCTTCTACTTCTAGCCAGACAGCGGCC 730
 Qy 102 roArgSerTTPCysLeuArgThrValCysAsnProTTPPheGluArgValSerMetLeuV 122
 Db 731 CGCGAGAGTGGTGTCTCCGACCGCTGTGTAAACCCCTGGTGTAGCGCATCAGCATGTGG 790
 Qy 122 alileLeuLeuAasnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
 Db 791 TCATCTCTCACTCGGTGACCTGGGCATGTTCCGGCCATCGGAGGACATCGCTGTG 850
 Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlav 162
 Db 851 ACTCCAGCGCTCGCGATCCTCGAGGCTTTCATGATCACTTCTCTTCTTCTTCTTCTGCG 910
 Qy 162 alGluMetValValLysMetValAlaLysGlyIlePheGlyLysLysCysTyrLeuGlyA 182
 Db 911 TGAGAGATGGTGGTGAAGATGGTGGCTTGGGCATCTTTGGGAAAGAGTGTATTACCTGG 970
 Qy 182 spThrTTPAasnArgLeuAspPheIleValIleAlaGlyMetLeuGlyTyrSerLeuA 202
 Db 971 ACATTTGGAAACCGGCTTGACTTTTTCATCTCATCGCAGCGGATGCTGGAGTACTCGCTGG 1030
 Qy 202 spLeuGlnAasnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
 Db 1031 ACCTGAGAACGTCAGCTTCTCAGTGTAGGACAGTCCGTGTGTCGACGACCGCTCAGGG 1090
 Qy 222 laileAasnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM 242
 Db 1091 CCATTAAACCGGGTCCCGAGCATCGCATCTTGTACGTTGCTGTGAGTACGCTGGCCCA 1150
 Qy 242 etLeuGlyAasnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV 262
 Db 1151 TGTGGGCAACGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1210
 Qy 262 alGlnLeuTTPAlaGlyLeuLeuAasnArgCysPheLeuProGluAasnPheSerLeuP 282
 Db 1211 TCCAGCTGTGGCAGGCGCTCTTCGGAACCGATGCTCTCTTCTCTCTCTCTCTCTCTCT 1270
 Qy 282 roLeuSerValAapLeuGluProTyrTyrGlnThrGluAasnGluAapGluSerProPheI 302
 Db 1271 CCCTGAGCGTGGACCTGGAGCGCTATTATCCAGACAGAGAGACGAGGATGAGAGCCCTTCA 1330
 Qy 302 leCysSerGlnProArgGluAasnGlyMetArgSerCysArgSerValProThrLeuArgG 322

Db	1331	TCTGCTCCAGCAGCAGCGAGAACGGCATGCGGTCTCTGCAGAAAGCGTGCACCGCTGCGCG	1390	Db	2411	GCTCCATGCACAGCTGCTGGAGACACAGAGTACAGGTGCTGCCAAAGCTCTTTGCAAGA	2470
Qy	322	lyGluGlyGlyGlyGlyProCysSerLeuAspTyrGluThrTyrAsnSerSerA	342	Qy	682	leSerSerProCysSerIleAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	1391	GGGACGGGGGGGTGGCCACCTTGCGGTCTGGACTATGAGCCCTACACAGCTCCAGCA	1450	Db	2471	TCTCAGCCCTTGCTTGAAGACAGACAGTGGAGCTGTGTGCTCCAGACAGCTGCCCTACT	2530
Qy	342	snThrThrCysValAsnTyrAsnGlnTyrTyrAsnCysSerAlaGlyGluHisAsnP	362	Qy	702	ysAlaAargThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspS	722
Db	1451	ACACCACTGTGTCACTGGAACCACTACTACACCAACTGCTCAGCGGGGAGCACAACC	1510	Db	2531	GTGCCCGGGCGGGGAGGGAGGTGGAGCTGCCGACCGCTCGGGAGCCCCACA	2590
Qy	362	rpPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaIlePheGlnV	382	Qy	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuAargAspProHisS	742
Db	1511	CCTTCAAGGGCGGCATCAACTTTGACAACTTGGCTATGCTGGATCGCCATCTTCCAGG	1570	Db	2591	CGAGGCGAGTTTATGAGTTTACACAGGATGCCAGCAGCAGCCTCGGGAGCCCCACA	2650
Qy	382	alrIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSerPheT	402	Qy	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	1571	TCAATCAGCTGGAGGGCTGGGTGGCATCATGTACTTGTGTGATGATGCTCATCTCTTCT	1630	Db	2651	GC---CGCGCGCAACGGAGCGCTGGGCCAGATGGAGAGCCAGCTCTGTGTGGCCTTCT	2707
Qy	402	YrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC	422	Qy	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	1631	ACAATTTCACTACTCTCTCTCATCATCTGCGGCTCTTCTTTCATGATCAACCTGT	1690	Db	2708	GGAGGCTAATCTGTGACACCTTCGAAAGATTTGGACAGCAAGTACTTTTGGCGGGGAA	2767
Qy	422	YsLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442	Qy	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	1691	GCCTGGTGGTATGTCAGCGAGTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATGC	1750	Db	2768	TCATGATGCCATCTGTCGTCACACACTCAGCATGGGCATCGAATACCAGCAGCAGCCG	2827
Qy	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462	Qy	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	1751	GGAGAGCGCTGTGGGTTCCTGTCACCGCAGCACCTTGGCTAGCTTCTGTAGCCCG	1810	Db	2828	AGGAGCTTACCAACGCCCTAGAAATCAGAACATCGTCTTACCAGCCTCTTTGGCCTGG	2887
Qy	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAArgA	482	Qy	822	luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Db	1811	GCAGCTGCTATGAGGAGCTCTCAAGTACCTGCTGTACATCTCTCGTCCACCGCGCTAT	1870	Db	2888	AGATCTGCTGAGCTGCTGTGTATGTCCTTGGCTACATCAAGAATCCCTACAACA	2947
Qy	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502	Qy	842	lePheAspGlyValIleValIleSerValTyrGluIleValGlyGlnGlnGlyG	862
Db	1871	GGTGGCTCAGGTCTCTCGGGCAGCAGGTGCGGGTGGCTGCTCAGCAGCCAGCAC	1930	Db	2948	TCTTCGATGGTGTCAATTTGGTGTATCAGCTGTGGAGATCGTGGGCAGCAGGGGGCG	3007
Qy	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522	Qy	862	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	1931	CCCTCGGGGGCCAGGACCCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCGCTAT	1990	Db	3008	GCCTGTGGTGTGGGACCTTCCGCTGTATGCGGTGTCTGAAAGCTGTGGTGGCTTCTTGC	3067
Qy	522	erValHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis	542	Qy	882	roAlaLeuGlnArgGlnLeuValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	1991	CCGTCCACCACTGGTGCACACACACACACACACACACACACACACACACACACAC	2050	Db	3068	CGCGCTGCAGCGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3127
Qy	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562	Qy	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
Db	2051	GGAGCCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGATGCCAATGGGTCCC	2110	Db	3128	GCATGCTGCTTATGCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCT	3187
Qy	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582	Qy	922	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Db	2111	GCAGGCTCATGCTGCCACCACTCGAGCGCTGCGCTCTCGGGGGCCCCCGCTGGTGGCG	2170	Db	3188	GCAGTTTGGCTTCTGAGCGGGATGGGACACCTTGCAGACCGGAAGATTTTGACTCCT	3247
Qy	582	laGluSerValHisSerPheTyrHisHisHisHisHisHisHisHisHisHisHis	602	Qy	942	euLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	962
Db	2171	CAGAGTCTGTGCAGCTTCTACCATGCCACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2230	Db	3248	TGCTCTGGGCCCATCGTCACTGTCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCT	3307
Qy	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622	Qy	962	euTyrAsnGlyMetAlaSerThrSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT	982
Db	2231	CGCCCCCTCCAGGTCCTCCATCTCAGGCATCCGCGAGCCTGTGGCGAGCGGGAAGGTGT	2290	Db	3308	TCTACAAATGGTATGGCTCCAGTCTCTGGCGGCCCTTTTATTTCAITGGCCTCATGA	3367
Qy	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642	Qy	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	2291	ATCCACCGTGCACACCGCTCCACCGGAGAGCGCTGAAGGAGAGCGACTAGTAGAGG	2350	Db	3368	CCTTCGCAACTACGTGCTCTTCAATTTGCTGTGTCGCCATTTCTGTGGAGGGCTTCAGG	3427
Qy	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662	Qy	1002	laGlu-----	1003
Db	2351	TGGCTGCCAGCTCTGGGGCCCCCAACCTTCACAGCCTCAACATCCACCGGGGCCCTACA	2410	Db	3428	CGGAGGAAATACAGAAACCGGGAAGATGCGAGTGGACAGTTAAGCTGTATTTCAGCTGCTG	3487
Qy	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682	Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS	1019
				Db	3488	TCGACTCCCGAGGGGGAGATGCCAACAGTCCGAAATCAGAGCCCGATTTCTTCTCACC	3547


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Db      5705  |||||CCCCAGGTGGGAACTCTCTTCAATGTTGTTTTCATCTTGAG 5764
Qy      1759  laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db      5765  CTCCTGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTCTGAGGGCC 5824
Qy      1779  euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals 1799
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Qy      1799  erThrGlyAspAsnThrAsnGlyIleMetLeuAspProSerArgAspCysAspGlnGluS 1819
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Qy      1819  erThrCysIleAsnThrValIleSerProIleThrPheValSerPheValLeuThrAlaG 1839
Db      5945  CCACCTTGCTACACACGGTCACTCGCCTATCTACTTGTGTCTTGTGCTGACGGGCC 6004
Qy      1839  lnPheValLeuValAsnValIleAlaValLeuMetIleValMetIleValMetIleValMet 1859
Db      6005  AGTTCTGTCTAGTCAACGTTGATCGCGTGTCTGATGAAGCACCTTGGAGGAGAGCAACA 6064
Qy      1859  ysGluAlaIleGlyGluAlaGluLeuGluAlaGluLeuGluMetIleValMetIleValMet 1879
Db      6065  AGAGAGCCAAAGGAGGAGCGAGCTAGAGCTGAGCTGAGCTGGAGCTGGAGATGAAGACCTCA 6124
Qy      1879  erProGlnProHisSerProLeuGlySerProPheLeuThrProGlyValGluGlyValA 1899
Db      6125  GCCCCAGACCCCACTCGCCACTGGGAGCCCTTCTCTGGCTGGGGTTCGAGGGGCCCG 6184
Qy      1899  snSerThrAspSerProLysProGlyValAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
Db      6185  ACAGCCCCGACAGCCCCCAAGCTTGGGCTCTGCACCCAGCGGCCACCGAGATCAGCCT 6244
Qy      1919  erGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProL 1939
Db      6245  CCACCTTTTCCCTGGAGCACCCACGATGACGAGCCACCCACCGAGCTGCCA----- 6297
Qy      1939  euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA 1959
Db      6298  --GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTTCAGCCGAACGCACTCTCTGCCCA 6355
Qy      1959  snAspSerThrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979
Db      6356  ATGACAGTACATGTGCGCATGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCT 6415
Qy      1979  rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT 1999
Db      6416  GGGGGCTCCCCAAAGCTCAGTCAGCTCCGTCCTTGTTCGTTCACTCCAGCCAGCAGATA 6475
Qy      1999  hrSerCysIleLeuGlnLeuProLysAspValHisThrLeuLeuGlnProHisGlyAlap 2019
Db      6476  CCAGCTACATCTCTGAGCTTCCCCAAGATGACCTCATCTGCTCCAGCCCCCAGCGGCC 6535
Qy      2019  roThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgP 2039
Db      6536  CAACCTGGGGCACCATCCCCAACTGCCCCCAGCAGCGCTCCCTTTGGCTCAGAGGC 6595
Qy      2039  roLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerA 2059
Db      6596  CACTCAGCGCCGAGCAGCAATAAGGACTGCTCTTGGACGTTTCAGGGTCTGGCGAGCC 6655
Qy      2059  rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerP 2079
Db      6656  GGGAGAGCTCTGTCGAGAGTGGGCTCCCTCCCGCCCTCCCGCCCTTCTCTTCTTCTTCT 6715
Qy      2079  heTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL 2099
Db      6716  TCTGGGGCCAGTCAAGTACCCAGGACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCA 6775
Qy      2099  ysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp 2119

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Db      6776  AGCACATGACCCCGCCAGCCCTTGTCCAGGCGCCAGAACCACTGGGCAAGGGCCCTC 6835
Qy      2119  roGluThrArgSerSerLeuLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL 2139
Db      6836  CAGAGACCAGAGCAGCTTAGAGTTGACACGGAGCTGAGCTGGATTTCAGGAGACCTCC 6895
Qy      2139  eu---ProSerSerGlnGluProLeuPheProArgAspLeuLeuLysCysTrpSerV 2158
Db      6896  TGCCCCCTGGCGCCAGAGAGGCCCTCCATCCACCGGACCTGAAGAAGTGTCTACAGCG 6955
Qy      2158  alGluThrGlnSerCysArgArgProGlyPheThrLeuAspGluGlnArgHis 2178
Db      6956  TGGAGGCCAGAGCTGCGAGCGCGGCTAGCTCTGGCTGGATGACAGAGGAGACACT 7015
Qy      2178  erIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerS 2198
Db      7016  CTATCGCGCTGAGCTGCTGGACAGCGCTCTCCAAACCCACCTGGGCGACAGACCCCTCTA 7075
Qy      2198  erLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProp 2218
Db      7076  ACCTTGGGGCGCAGCTCTTGGGGGCCCGGAGCGGCCCAAGAAAAAATCTCAGCCCGC 7135
Qy      2218  roSerIleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyV 2238
Db      7136  CTAGTATCACCATAGACCCCGGAGAGCCAAAGTCTCGGACCCCGCCCTGGCTGTGTA 7195
Qy      2238  alCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProL 2258
Db      7196  TCTGCTCTCGAGAGAGGCTCTGCTCCAGGACTCCAGGATCCCTTGGCCCTCTGGCCCC 7255
Qy      2258  euAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuS 2278
Db      7256  CTGACAGCATGCTCGCTCGCCCTCCCAAGAAAGATGTGTGAGTCTCTCCGGTTTAT 7315
Qy      2278  erSerAspProThrAspMetAspPro 2286
Db      7316  CCTCTGACCCAGCAGACCTGGACCCC 7341

RESULT 9
AA83481
ID AAX83481 standard; cDNA; 6750 BP.
XX
AC AAX83481;
XX
XX 07-DEC-1999 (first entry)
DT
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1a) cDNA.
XX
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
XX WO9929847-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
XX 05-DEC-1997; 97US-00985809.
PR
XX
XX (LOYO ) UNIV LOYOLA CHICAGO.
PA
XX
XX Perez-Reyes E, Cribbs LL;
PI
XX
XX WPI; 1999-394972/33.
DR P-PSDB; AAY14586.
XX
XX New T-type voltage-gated calcium channels.
PT
XX
XX Disclosure; Page 31-40; 138pp; English.
PS
XX
XX This sequence represents the coding region for a human T-type voltage-
CC

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Qy	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCCTCTTCATCTTCGGGCATCGTCGGGCTGCAGCTGTGGCAGGGCTGCTTCGGAACCCGAT	721
Qy	273	ysPheLeuProGluuAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722	GCCTTCCTACCTGAGAAATTTTCAGGCTCCCCCTGAGCGTGGACCTGGAGCGCTATTACCAGA	781
Qy	293	hrGluuAsnGluuAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAACGAGGATGAGAGGCCCTTCATCTGCCTCCAGCCACGCGAAGCGGATGCGGT	841
Qy	313	erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGCAGAACGCTGCCACACCTCGCGGGACGCGGGCGGTGGCCACCTTCGCGGTCTGG	901
Qy	333	spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
Db	902	ACTATGAGGCCATACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTACA	961
Qy	353	hrPheCysSerAlaGlyGluuHisAsnProPheIleGlyAlaIleAenPheAsnIleG	373
Db	962	CCAACCTGCTCAGCGGGGAGACAAACCCCTTCAAGGCGGCATCAACTTTGACAACATTC	1021
Qy	373	lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT	393
Db	1022	GCTATGCTGGATCGCATCTTCAGGTCATCAGCTGGAGGGCTGGTGCACATCATGT	1081
Qy	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV	413
Db	1082	ACTTTGTGATGGATGCTCATCTCTTACAAATTTCTACTACTTCATCTCTCATCATCG	1141
Qy	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCCCTTCTCATGATCAACTGTGCTGGTGGTATGGCCACGAGTTCTTCAGAGA	1201
Qy	433	hrlYsGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas	453
Db	1202	CCAAGCAGCGGGAAGCCAGCTCATCGGGAGCAGCGTGTGCGGTTCTGTCCAACGCCA	1261
Qy	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuIleYsTrLeuV	473
Db	1262	GCACCTTGGCTAGCTTCCTCTGAGCCCGGAGCTGCTATAGAGAGCTGCTCAAGTACCTCG	1321
Qy	473	alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTACATCCTTCGTAGGACGCCGAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC	1381
Qy	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGGAGACCACGCCCAGCAGCA	1441
Qy	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
Db	1442	GCTGCTCTCGCTCCCAACCGCGCTATTCGCTGCACCACTCTGGTGACACCAACCCACC	1501
Qy	533	ishHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ATCACCACTACCTACCACTGGCAATGGGACGCTCAGGGGCCCCCGGGCCAGCCCGGAGA	1561
Qy	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT	573
Db	1562	TCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGCTGCCACCACTCTCGACGGCTG	1621
Qy	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
Db	1622	CCCTCTCCGGGGCCCCCTTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCGGACT	1681
Qy	593	ysHisLeuGluProValArgCysGlnAlaProProProProArgCysProSerGluAlaSerG	613
Db	1682	GCACTTAGAGCAGTCCGCTGCGAGCGGCCCTCCAGGTCCCATCTCTGAGGCATCCG	1741

QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
DB 1742 GCAGGACTGTGGGACGCGGAAGGTATCCACCGTGCACACCGCCCTCCACCGGAGA 1801
QY 633 leuLeuAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
DB 1802 CGCTGAAGGAGGAGGACCTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
DB 1862 GCCTCAACATCCACCGCGCCCTACAGCTCCATGCACAACTGTGTGGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
DB 1922 CAGGTGCTGCCAAGACTCTTCAAGATCTTCAGGATCTTCAGGCTTGTGAAAGCAGACAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
DB 1982 CTTGTGCTCAGACAGCTGCCCTACTGTGCCGGCGGGCAGGGAGGTGGAGCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
DB 2042 CCGACCGTGAAATGCTGACTCAGACAGCGAGCAGTTTATGATTTCAACAGGATGCC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
DB 2102 AGCACAGCGACCTCCGGGACCCCAACAGC---CGGCGGCACAGGACCTGGGCCCCAGATG 2158
QY 753 laGluProSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
DB 2159 CAGAGCCAGCTCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
DB 2219 TGGACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTCTGTGTCACACACTCAGCA 2278
QY 793 etGlyIleGluTyrHisGluInProGluLeuThrAsnAlaLeuGluIleSerAsnI 813
DB 2279 TGGGCATCGAATACACAGACGCCCGAGAGCTTACCAACGCCCTTAGAATCAGGACAA 2338
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProP 833
DB 2339 TCGTCTTCCACGACCTCTTTGCTGGAGATGCTGTGAAGCTGTGTGTATGTGTCCT 2398
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
DB 2399 TTGGCTACATCAAGAATCCCTACAACATCTTCGATGGTGCATTTGGTTCATCAGCGTGT 2458
QY 853 rpGluIleValGlyGlnGlnGlyGlyValLeuSerValLeuArgThrPheArgLeuMetA 873
DB 2459 GGGAGATCTGTGGCCAGCAGGGGGGGCGCTGTGCGTGTGCGGACCTTCCGCTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
DB 2519 GTGTGCTGAAGCTGTGCTGCGCTTCTGCGCGCGCTGCAGCGCAGCTGTGTGCTCATGA 2578
QY 893 ysrMetAspAsnValAlaThrPheCysMetIleLeuMetLeuPheIlePhePheS 913
DB 2579 AGACCATGGCAACGTCGGCCACCTTCGACGTGCTTATGCTCTTCATCTTCA 2638
QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
DB 2639 GCATCTTGGCATGCACTCTTTCGGCTGCAAGTTTGGCTCTGAGCGGATGGGACACCC 2698
QY 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
DB 2699 TGCCAGACCGGAAGATTTTGACTCTTGTCTGGGCGCATCGTCACTGCTTTTCAGATCC 2758
QY 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpA 973
DB 2759 TGACCCAGGAGGACTGGAAACAAAGTCTCTACATGATGTATGGCTCCACGCTGCTCTGGG 2818
QY 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993

DB 2819 CGGCCCTTATTTTATTCATTCGCCCTCATGACCTTCGCAACTACGTCTCTTCAATTGCTGG 2878
QY 993 alAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
DB 2879 TCGCATTTCTGTTGGAGGCTTCCAGCGGAGGAGATGCCAACAAAGTCCGAATCAGAGC 2938
QY 1013 roAspPhePheSerProSerValAspGlyAspGlyAspAtqLysLysArgLeuAlaLeuV 1033
DB 2939 CCGATTTCTTCCACCGAGCTGTGATGGGACAGGAAGAGTGTTCGCTTGG 2998
QY 1033 alAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT 1053
DB 2999 TGTCCCTGGAGAGACCCCGAGCTGCGAAGAGCCTGCTCCGCTCTCATCTCCACA 3058
QY 1053 hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG 1073
DB 3059 CGGCCGACACCCATGTCGTGCTGCCAAGACAGCAGCAGCGGGCTGGCGAGGCGCTGG 3118
QY 1073 lySerGlySerArgThrSerSerGlySerAlaGluProGlyAlaAlaHisHisG 1093
DB 3119 GCCTGCTCGCGCCGACACAGCAGCGGTGGCAGAGCTGGGCGGCC---CAGC 3175
QY 1093 luMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
DB 3176 AGATGAAGTCAACCGCCAGCGCCGAGCTCTCCGACACAGCCCTGGAGCGCTGCAAGCA 3235
QY 1113 erTrpThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
DB 3236 GCTGACACAGAGGCGCTCCAGCGGAAACAGCTCGCGCGTGCACCCAGCTTGAAGCGGA 3295
QY 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG 1153
DB 3296 GNAAGCCCAAGTGGAGAGCGCGGTCCCTGTGTGCGGAGAGGCCAGAGAGCCAGGATG 3355
QY 1153 luGluLysSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
DB 3356 AAGAGGAGAGCTCAGAGAGGAGCGGCGAGCTTGCAGGAGTACCATGCCACAGG 3415
QY 1173 lySerLeuGluArgGluAlaLysSerPheAspLeuProAspThrLeuGlnValProG 1193
DB 3416 GGTCTCTGAGCGGAGGCGCAAGAGTCTCTTTGACTGCCAGACACACTGCAAGTGCAG 3475
QY 1193 lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
DB 3476 GGTCTCATCGCACTGCCAGTGGCGGAGGTCTGCTTCTGAGCACCGAGGACTGCAATGGCA 3535
QY 1213 ysrAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
DB 3536 AGTCGGCTTCAGGGCGCTTGGCGCGGCTGATGACCCCGCTGATGACCCCGCTGGATGGG 3595
QY 1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
DB 3596 ATGACCGCATGACAGGCGCACTTGCAGCAAGGGAGCGGTCCGCGCTGGATCCGAG 3655
QY 1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
DB 3656 CCGACTCTCCCTGCTGCTGCTCGAGCGAGACTCTCTGTGTGAGCTTCTTCCCTCTTC 3715
QY 1273 lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
DB 3716 AGTCCAGGTTCGCGCTCTGTGTACCGGATCATCACCCACAGATGTTTCGACCGCTGG 3775
QY 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313
DB 3776 TCTTGTCTCATCTCTTCTTACTGATCACCATCGCCATGGAGGCGCCCAAAATGGAC 3835
QY 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
DB 3836 CCACAGCGCTGAACGCACTCTTCTGACCTCTTCCAAATTAATCTTTCACCGCAGTCTTTC 3895
QY 1333 euAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrL 1353

QY 2073 euThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnArgSerGlyI 2093
 DB 6107 TGGCCCGGCGCTACTCTTTCTGGGGCCAGTACAGGACGACGAGCACTCCCGCA 6166
 QY 2093 leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
 DB 6167 GCACAGCAAGATCTCAAGACATGACCCCGCAGCCCTTGGCCAGGCCAGAACCA 6226
 QY 2113 exTrpAlaLysAspProProGluThrArgSerSerIleGluLeuAspThrGluLeuSerT 2133
 DB 6227 ACTGGGGCAAGGGCCCTCCAGAGACAGAAAGCAGCTTAGAGTTGGACACGGAGCTCAGCT 6286
 QY 2133 rPileSerGlyAspLeuLeu---ProSerSerGlnGluProLeuPheProArgAspL 2152
 DB 6287 GGATTTTCAGAGACCTCTCTGCCCTTGGCGGCGGAGGAGGCCCCATCCCCACCGGACC 6346
 QY 2152 euLysLysCysTrpSerValGluThrGlnSerCysArgArgProGlyPheTrpLeuA 2172
 DB 6347 TGNAGAGTGTCTACAGCTGGAGGCCAGCTGCCAGCGCGGCTACGTCTCTGGCTGG 6406
 QY 2172 spGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgL 2192
 DB 6407 ATGAGCAGAGGAGACACTCTATCGCGTCTAGCTGCTGGACAGCGGCTCCCAACCCACC 6466
 QY 2192 euCysProSerProSerSerLeuGlyGlnProLeuGlyProGlySerArgProL 2212
 DB 6467 TGGGCACAGACCCCTCTAACCTTGGGGGCGGAGGCTTGGGGGCGCTGGAGCGGCGCCA 6526
 QY 2212 ysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgP 2232
 DB 6527 AGAANAACCTCAGCCCGCTAGTATCACCATAGACCCCCCGAGAGCCAAAGGTCTCTCGGA 6586
 QY 2232 roProCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspP 2252
 DB 6587 CCCCGCCAGCCCTGTATCTGCTCGGAGGAGGCTCGCTCCAGCGACTCCAGGATC 6646
 QY 2252 roSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrL 2272
 DB 6647 CCTTGGCCTCTGGCCCCCTTGACAGATGCTGCTCGCTCGCCCTCCCAAGAGATGTGC 6706
 QY 2272 euSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
 DB 6707 TGAGTCTCTCGGTTTATCTCTGACCCAGCAGACCTGGAGCCCC 6750

RESULT 10
 ID AAX83483
 AC AAX83483 standard; cDNA; 6804 BP.

XX AC AAX83483;

XX DT 07-DEC-1999 (first entry)

XX DE Human T-type voltage-gated Ca channel alpha-1-G (hCavTic) cDNA.

XX KW Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX OS Homo sapiens.

XX FN WO9929847-A1.

XX PD 17-JUN-1999.

XX PF 30-OCT-1998; 98WO-US023161.

XX PR 05-DEC-1997; 97US-00985809.

XX PA (LOYO) UNIV LOYOLA CHICAGO.

XX PI Perez-Reyes E, Cribbs LL;

XX DR WPI; 1999-394972/33.

XX P-PSDB; AAY14588.

XX New T-type voltage-gated calcium channels.
 PS Disclosure; Page 49-58; 138pp; English.
 CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavTic. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

SQ Sequence 6804 BP; 1301 A; 2186 C; 1998 G; 1319 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 6804
 Score: 10946.00 Matches: 2110
 Percent Similarity: 94.20% Conservative: 32
 Best Local Similarity: 92.79% Mismatches: 106
 Query Match: 91.00% Indels: 26
 DB: 2 Gaps: 5

US-09-611-257A-24 (1-2287) x AAX83483 (1-6804)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
 DB 2 TGGACGAGGAGGAGATGGAGCGGCGCGAGGAGTCCGGACAGCCCGGAGCTTCATGC 61
 QY 54 SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGluLysAspP 73
 DB 62 GGCTCAACGACCTGTCCGGGGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
 QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyPrProAlaLeuAlaProValValP 93
 DB 122 CGGGCAGCGCGACTCCGAGGCGGAGGGGCTGCCCTACCGCGCGCTGGCGCGGTTT 181
 QY 93 hePheTyrlLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
 DB 182 TCTTCTACTTGAGCCAGGACAGCCCGCGGAGCTGGTGTCTCCGACGGTCTGTAAACC 241
 QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
 DB 242 CCTGGTTTGGCGCATCAGCATGTTGGTCTCTCTCACTCGGTGACCCCTGGGCATGT 301
 QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
 DB 302 TCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCCGATCTCTGCGAGCCTTTG 361
 QY 153 spAspPheIlePheAlaPheAlaValGluMetValValLysMetValAlaLeuGlyI 173
 DB 362 ATGACTTCATCTTTCCTTTTGGCGTGAGATGGTGGTGAAGATGGTGGCTTGGGCA 421
 QY 173 lePheGlyLysLysCysTyrlLeuGlyVAspThrTrpAsnArgLeuAspPheIleValI 193
 DB 422 TCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGTACTTTTTCATCGTCA 481
 QY 193 leAlaGlyMetLeuGluTyrlSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
 DB 482 TCGCAGGAGTGTGGAGTACTCGCTGGACCTGCAGAACGCTCAGCTTCTCAGCTGTGAGGA 541
 QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

Db 542 CAGTCGCTGCTGCGACCGCTCAGGCGCAATTAACCGGGTGCCAGCATGCGCATCTTG 601
 Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
 Db 602 TCAGCTTGCTGCTGCGATACGCTGCCATGCTGGGCAACGCTCCTGCTCTGCTCTTCG 661
 Qy 253 alPhePheLeuPheGlyLeuValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgC 273
 Db 662 TCCTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAAGGCTGCTTCGGAAACCGAT 721
 Qy 273 ysPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
 Db 722 GCTTCCTACCTGAGATTTACAGCTCCCGCTGAGCGTGGACCTGAGCGCTATTACCA 781
 Qy 293 hrGluAsnGluAspGluSerProPheLeuLeuCysSerGlnProArgGluAsnGlyMetArgS 313
 Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGGT 841
 Qy 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 333
 Db 842 CCTGCAGAGCGTCCACAGCTGCGCGGGACGCGGGGGTGGCCACCTTGCGGTCTGG 901
 Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyrT 353
 Db 902 ACTATGAGGCTTACACAGCTCCAGCAACACCTGCTGTCAACTGGAACCCAGTACTACA 961
 Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLeuGlyGlyGlyGlyGlyGlyGlyGlyGly 373
 Db 962 CCAACTGCTCAGCGGGGGAGCACAACTTCATAGGGGGCGCATCAACTTTGACAAACATG 1021
 Qy 373 lyTyrAlaTyrPheAlaLeuPheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
 Db 1022 GCTATGCTGGATCGCCATCTTCCAGGTATCATGCTGGAGGGTGGGTGCATCATGT 1081
 Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleLeV 413
 Db 1082 ACTTTGTGATGATGCTCATCTTCTTACAAATTTCTACTTCTCATCTCTCTCATCATCG 1141
 Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
 Db 1142 TGGGCTCTCTTCTCATGATCAACCTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1201
 Qy 433 hrLyGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlas 453
 Db 1202 CCAAGCAGCGGGAAGCAGCTGATGCGGAGCAGCGTGTGCGGTTCCTGTCCAACGCCA 1261
 Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
 Db 1262 GCACCTCTGGCTAGCTTCTTGAGCCCGGAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
 Qy 473 alTyrIleLeuArgGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
 Db 1322 TGTACATCTCTTCTGTAAGCAGCCCGCAGGCTGGCTCAGGCTCTCTCGGGCAGCAGGTGTC 1381
 Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
 Db 1382 GGGTTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGGCCAGAGACCCAGCCCGCAGCAGCA 1441
 Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
 Db 1442 GCTGCTCTCGCTCCACCGCGCTATCTCGTCCAGCACCTGCTGGTGCACCCACCCACCC 1501
 Qy 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
 Db 1502 ATCACCACCACTACACCTGGGCAATGGAGCGCTCAGGGCCCGCGGCGCCAGCGCGGAG 1561
 Qy 553 leGlnAspArgAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
 Db 1562 TCCAGGACAGGATGCGCAATGGGTCCCGCGGCTCATGCTGCCACCACTCTCGACGCGCTG 1621
 Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTTACCATGCCGACT 1681
 Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
 Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCCATCTGAGGCATCCG 1741
 Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
 Db 1742 GCAGGACTGTGGCAGCGGAGAGGTGTATCCACCGTGCACACCAGCCCTCCACCGGAGA 1801
 Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProProThrLeuThrs 653
 Db 1802 CGCTGAAGAGAGGACACTAGTAGAGGTGGCTGCAGCTCTGGGCCCCCAACCTCCACCA 1861
 Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
 Db 1862 GCCTCAACATCCACCGGGCCCTTACAGCTCCATGCAACAGTCTGTGGAGACACAGAGTA 1921
 Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
 Db 1922 CAGGTGCTGCCAAAGACTCTTCAAGATCTCCAGCCCTTGTTCGAAAGCAGACAGTGGAG 1981
 Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
 Db 1982 CTTGTGTCAGACAGCTGCTGCTCTTCTGTCGCGGGCGGGCAGGGGAGGTGAGCTCG 2041
 Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
 Db 2042 CCACCCGTGAATTCCTGACTCAGACAGCAGGAGGAGTTTATGAGTTTCAACAGATGCC 2101
 Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
 Db 2102 AGCACAGCAGCTCCGGGACCCCCACAGC -- CGCGCGCAACCGAGCGTGGGCCAGATG 2158
 Qy 753 laGluProSerSerValLeuAlaPheThrPheArgIleCysAspThrPheArgLysIleV 773
 Db 2159 CAGAGCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2218
 Qy 773 alaSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
 Db 2219 TGACAGCAAGTACTTTGGCGGGGAAATCATGATCGCCATCTCTGGTCAACACATCAGCA 2278
 Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
 Db 2279 TGGCATCGAATACCAGCAGCAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
 Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProp 833
 Db 2339 TCGTCTTACACAGCCTCTTGGCTGGAGATGCTGCTGAAAGCTGCTGTGTGTGCTGCT 2398
 Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
 Db 2399 TTGGCTACATCAGAAATCCCTTACAACATCTTCGATGGTGTCAATGGTCAATCAGCGTGT 2458
 Qy 853 rpGluIleValGlyGlnGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG 873
 Db 2459 GGGAGATCGTGGCCAGCAGCGGGGGCGCTGTGCGTGTGCTGCGGACCTTCGCGCTGATGC 2518
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RESULT 11
AA83482
ID AA83482 standard; cDNA; 6783 BP.
AC
AA83482;
XX
07-DEC-1999 (first entry)
XX
Human T-type voltage-gated Ca channel alpha-1-G (hCavT1b) cDNA.
XX
Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX
activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
Homo sapiens.
XX
WO9929847-A1.
XX
17-JUN-1999.
XX
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 QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
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 QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
 Db 722 GCTTCTACCTGAGATTTTACGCTCCCTCGAGCGTGGACCTGGAGCGCTATTACCGA 781
 QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
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 QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
 Db 842 CTTGCAAGAGGTGCCACGCTGCGGGGACGGGGCGGTGGCCACCTTGGCGTCTGG 901
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 QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT 433
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 QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
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Qy 1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
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QY 498 eSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
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QY 518 ieArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHis 538
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DB 4321 TCATTTTTCGCACTCTTGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTGTCGACGGCG 4380
QY 1455 luAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValA 1475
DB 4381 AGGATACAGGAACATCACCAATAAATTCGAGCTGTGCGGAGGCGAGTTTACCGTGGGTCC 4440
QY 1475 rgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlas 1495
DB 4441 GGCACAAGTAAACTTTGACAACCTTGGCCAGGCGCTGATGTCCTGTTGTTTGGCCT 4500
QY 1495 erLysAspGlyTTPValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnG 1515
DB 4501 CCAAGGATGTTGGTGGACATCATGTACGATGGCTGGATGCTGTGGGCGTGGACCGC 4560
QY 1515 lnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleV 1535
DB 4561 AGCCCATCATGAACACACACCCCTGGATGTGTGTTACTTCTTCATCTGCTCTGCTCATTTG 4620

QY 1535 alAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysA 1555
DB 4621 TGGCCTTCTTTGCTTCTGAACATGTTTGGTGGTGGTGGTGGAGAACTTCCACAAGTGTA 4680
QY 1555 rgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuG 1575
DB 4681 GGCAGCACAGGAGGAGGAGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4740
QY 1575 luLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrS 1595
DB 4741 AGAAAAGAGAAGG-----AAAGCCAGTGCACACCTTACTACT 4779
QY 1595 erAspTyrSerArgPheArgLeuValHisHisLeuCysThrSerHisTyrLeuAspL 1615
DB 4780 CCGACTACTCCCGCTTCGCGCTCTCGTCCACCACCTTGTGCACCAGCCACTACTCGGACC 4839
QY 1615 euPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnG 1635
DB 4840 TCTTCATCAGAGGTGTATCGGCTGAACGTGTGTCCATCGGCTGAGGAGGAGGAGGAGGAGG 4899
QY 1635 lnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheV 1655
DB 4900 AGCCCCAGATTTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTCTTTG 4959
QY 1655 alPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgT 1675
DB 4960 TCTTGGAGTCAGTTTCAAACCTTGTGGCCTTGTGGTTCGCTCGGTTCTTCCAGGACAGT 5019
QY 1675 rpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluI 1695
DB 5020 GGAACAGCTGGACCTGGCCATTTGTCTGTCTCATCGGCTGAGGAGGAGGAGGAGGAGGAGG 5079
QY 1695 leGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuA 1715
DB 5080 TCAGAGTCAACGCTCGCTGCCCATCAACCCCACTCATCCGCATCATGAGGAGGAGGAGGAGG 5139
QY 1715 rgIleAlaArgValLeuLysLeuMetAlaValGlyMetArgAlaLeuLeuHisT 1735
DB 5140 GCATTCGCGAGTCTGAGGCTGCTGAAGTGGCTGTGGGCATGCGGGCGCTCTCGGACA 5199
QY 1735 hrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
DB 5200 CGGTGATGAGGCGCTCGCCAGTGGGAAACCTGGGACTTCTCTCATGCTGTGTGTGT 5259
QY 1755 heIlePheAlaLeuLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisP 1775
DB 5260 TCATCTTTCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTTGGAGTGTGAGGAGGAGGAGG 5319
QY 1775 roCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
DB 5320 CTTGTAGGCGCTGGGCGCTCATGCCACCTTTTCGGAACCTTGGCATGGGCTTCTTAACCC 5379
QY 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspC 1815
DB 5380 TCTTCCGAGTCTCCACAGGTGCAATTTGGAATGGCATTTATGAAGGACACCCCTCGGAGCT 5439
QY 1815 ysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheV 1835
DB 5440 GTGACAGAGGTCCACTGCTACACAGGCTCATCTCGGCTATCTACTTTGTGTCTTCG 5499
QY 1835 alLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG 1855
DB 5500 TGTGTAGCGGCCAGTTCGTGTAGTCAACGTGTGTATCGCGGTGCTGTATGATGAGGAGGAGG 5559
QY 1855 luGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluM 1875
DB 5560 AGGAGAGCAACAAGGAGGCGCAAGGAGGCGCGGCTAGAGGCTGAGCTGAGCTGAGCTGAGG 5619
QY 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1895
DB 5620 TGAAGACCTTCAGCCCCCAGCCCACTGCGCACTGGGAGGCGGCTTCTTCTTGGCCCTGGGG 5679
QY 1895 aGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisI 1915

SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7648
 Score: 10845.50 Matches: 2105
 Percent Similarity: 89.72% Conservative: 33
 Best Local Similarity: 88.33% Mismatches: 110
 Query Match: 90.17% Indels: 135
 DB: 13 Gaps: 7

US-09-611-257A-24 (1-2287) x ADQ89063 (1-7648)

Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
 Db 2 TGGACGAGGAGGATGGAGCGCGCCGAGGAGTCGGGACAGCCCGGAGCTTCATGC 61
 Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
 Db 62 GGCTCAACGACCTGTCGGGGCGCGGGCGCGCGCGGGGTGACGAGAAAGGACC 121
 Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValp 93
 Db 122 CGGGACGCGGAGCTCCGAGCGGAGGGGTGCGGTACCGCGCGCTGGCGCGGTGGTTT 181
 Qy 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
 Db 182 TCTTCTACTTGGACGACGAGCAGCGCGCGCGGAGCTGGTGTCTCCGACGGTCTGTAACC 241
 Qy 113 roTPPheGluArgValSerMetLeuValLeuLeuLeuAsnCysValThrLeuGlyMetP 133
 Db 242 CCTGGTTTGGCGCATCAGCATGTTGGTTCATCTCTCAACTGCGTGCACCTGGCGCATGT 301
 Qy 133 heArgProCysGluAspLeuAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
 Db 302 TCCGGCCATCGAGGACATCGCTGTGACTCCGACGCGTGGCGGATCTCGAGGCGCTTG 361
 Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
 Db 362 ATGACTTCATCTTGGCTCTTCTTCCGCTGGAGATGGTGAAGATGGTGGCTTGGGCA 421
 Qy 173 lePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
 Db 422 TCTTTGGGAAAAGTGTACCTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
 Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
 Db 482 TCGCAGGGATGCTGGAGTACTCGCTGGACCTGCGAAGCGTCAAGCTTCTCAGCTGTCA 541
 Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
 Db 542 CAGTCCGTGTGCTCGACCGCTCAGGGGCCATTACCGGGTGGCCAGCATGGGCATCTTGG 601
 Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
 Db 602 TCAGCTTGTGCTGGATACGCTGCGCCATGCTGGGCAACGCTCCTGCTGCTCTCTCTTC 661
 Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
 Db 662 TCTTCTTTCATCTTCGGCATCGTGGCGCTCCAGCTGTGGGAGGGCTCTTCGGAACCGAT 721
 Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
 Db 722 GCTTCTTACCTGAGAAATTTAGCTTCCCTTGACGCTGGACCTGGAGGGCTATTACCAGA 781
 Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
 Db 782 CAGAGAAGGAGATGAGAGCCCTTCTCTCTCCAGCCACCGAGAACGGCATGGCTCGGT 841
 Qy 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
 Db 842 CCTCAGAAAGCGTCCACACGCTGGCGGGGACGGGGCGGGTGGCCACCTTGGCGGTCTGG 901
 Qy 333 spTyrGluThrTyrAsnSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353

Db 902 ACTATGAGGCGCTACAAACAGCTCCAGCAACACCACTGTGTCAACTGGAACAGTACTACA 961
 Qy 353 hrAsnCysSerAlaGlyGlyUhiAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
 Db 962 CCAACTGCTCAGGGGGGAGCAAAACCCCTTCAAGGGCGGCATCAACTTTTGACAAACATTG 1021
 Qy 373 lyTyrAlaTAlaIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
 Db 1022 GCTATGCTGGATCGCATCTTCCAGGTCACTACGCTGGAGGGCTGGGTGCACATCATGT 1081
 Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleLeV 413
 Db 1082 ACTTTGTGATGGATGCTCATCTTCTTACAATTTCACTACTTCACTCTCATCATCG 1141
 Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
 Db 1142 TGGGCTCTCTTCTCATGATCAACCTGTGCTGGTGGTATGGCACGAGTCTTCAGAGA 1201
 Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
 Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGGGGAGCAGCGTGTGGTCTCTCGGCGACGAGTGTGC 1261
 Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
 Db 1262 GCACCTTGGCTAGCTTCTGTAGCCGCGAGCTGTATGAGGAGCTGCTCAAGTACCTGG 1321
 Qy 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
 Db 1322 TGTACATCTCTCGTAAGGAGCGCGAGCTGAGGTCTCTCGGCGACGAGGTGTGC 1381
 Qy 493 rglAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
 Db 1382 GGGTGGGCTGCTCAGCGGCCAGCACCTCTCGGGGCGCAGGAGACCCAGCCCGCAGCAGCA 1441
 Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
 Db 1442 GCTGCTCTGCTCCACCGCGCTATCGTCCACCACTGGTGTGCACCACTCCACCACTCC 1501
 Qy 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
 Db 1502 ATCACCACTACCTACCTCGGCAATGGGACGCTCAGGGGCCCCCGGGCGCAGCGGAGA 1561
 Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
 Db 1562 TCAGGACAGGATGCCAATGGTCCCGAGGCTCATGCTGCCACCACTCTCGACGGCTG 1621
 Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
 Db 1622 CCCTCTCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGACT 1681
 Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
 Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCTCATCTGAGGCATCCG 1741
 Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
 Db 1742 GCAGGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCACACCGGCTCTCCACCGGAGA 1801
 Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
 Db 1802 CGCTGAAGGAGAGGCACTAGTAGGGTGGCTGCCAGCTCTGGGCCCCCACTCCACCA 1861
 Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
 Db 1862 GCCTCAACATCCCAACCGGCGCTTACAGCTCCATGCACAAAGCTCTCGGAGACAGAGTA 1921
 Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
 Db 1922 CAGTGTCTGCCAAGAGCTTTCGAAGATCTCCAGCCCTTCTTGAAGAGCAGACAGTGGAG 1981
 Qy 693 laCysGlyProAspSerProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713

Db 1982 CCTGTGCTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGAGGGAGTGGAGCTCG 2041
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAATGCTGACTCAGACAGCGAGCAGTTTATGATTCACACAGGATGCC 2101
Qy 733 lnhisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGGACCTCCGGGACCCCAACAGC---CGGGGCAACGGAGCTGGGCCAGATG 2158
Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAAGCTGTGCTGGCCCTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACACAGACTACTTTGGCCGGGGAATCATGATCGCCATCTCTGGTCAACACACTCAGCA 2278
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCAACAGCAGCCGAGGAGCTTACCAACGCCCTAGAAATCAGAAACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProP 833
Db 2339 TCGTCTTTCACAGCCTTTTGGCCCTGGAGATGCTGCTGAAGCTGCTTGATGTCCT 2398
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT 853
Db 2399 TTGGCTACATCAAGATCCCTACACACTTTCGATGCTGTGCTATGCTTTCATCAGCGTGT 2458
Qy 853 rpGluIleValGlyGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGCAGATCGTGGGCCAGCAGCGGGGGCCCTGTGGTGTGCGGAGCTTCCGGCTGATGC 2518
Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTCTTGAACTGGTGGCTTCTCTCGCGGGCTGTCAGCGGAGCTGGTGTCTCATGA 2578
Qy 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCATGGCAACGCTGGCCACCTTCTGCATGCTGTCTTATGCTTCTTCTCATCTTCA 2638
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAlaArgAspGlyAspThrL 933
Db 2639 GCATCTCTGGGATGCATCTCTTTCGGCTGCAAGTTTGCTCTGACGGGATGGGACACCC 2698
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGATTTTGACTCTTGTCTCTGGGCCATCGTCACTGTCTTTCAGATCC 2758
Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
Db 2759 TGACCCAGGAGACTGGAAACAAAGTCTCTACAATGATGTATGGCTTCCACGTCGTCCTGGG 2818
Qy 973 laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTATTTATTCGCCCTCATGACTTTCGGCACTACGTGCTCTTCAATTTGCTGG 2878
Qy 993 alAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TCGCCATTCTGTGGAGGGCTTCCAGCGGAGGAAATCAGCAACCGGGAAGATCGCGATG 2938
Qy 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTTAAGCTGTATTACGTGCTGTGACTCTCCAGGGGGAGATGCCAACAGTCCG 2998
Qy 1010 luSerGluProAspPhePheSerProSerValAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGACCCGATTTCTTCTCACCCAGCTGGATGGTGATGGGACAGGAAGAAGTCT 3058
Qy 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuI 1050
Db 3059 TGGCCTTGTGTCTCTGGGAGAGCACCCGGAGCTGCGGAAGAGCTGTCTGCCGCTCTCA 3118

Qy 1050 leIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACACGCGCGCCACACCCATGCTGCTGCCAAGAGACACAGACGCGCTTGGCG 3178
Qy 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGGCGCTGGGCCCTCGCTCGCGCGCACACAGCAGCGGGTGCAGAGCTGGGGCGG 3238
Qy 1090 laHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA 1110
Db 3239 CC---CACGACATGAATCAGCGCCAGCGCCGAGCTCTCCGACACGCCCTTGAGCG 3295
Qy 1110 laAlaSerSerTrpThrSerArgArgSerArgAsnSerLeuGlyArgAlaProSerL 1130
Db 3296 CTGCAAGCAGCTGGACACAGCGGCTCCAGCGGACAGCTCGGCCGTGCACCCAGCC 3355
Qy 1130 euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluS 1150
Db 3356 TGAACGGGAGAACCCCAAGTGGAGAGCGGCTCCTGTTGTGGGAGAACGCCAGGAGA 3415
Qy 1150 erGlnAspGluGluSerSerGluAlaAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGGATCAAGAGAGAGCTCAGAAGAGAGCGCGGCCAGCCCTCGGGCAGTACCATC 3475
Qy 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGTTCCCTTGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGC 3535
Qy 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3536 AGTGTCCAGGGCTGCATCGCACTGCGAGTGGCGGAGGTCTGCTTCTGAGCACACAGGACT 3595
Qy 1210 ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCAATGGCAAGTGGCTTTCAGGGCGCTGCGCGGGCCCTGCGGCTGATGACCCCCAC 3655
Qy 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaT 1250
Db 3656 TGGATGGGATGACCGCGATGACAGGGCAACTGAGCAAAAGGGAACGGGTCCGCGCT 3715
Qy 1250 rpValArgSerArgLeuProAlaCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
Db 3716 GGATCGAGCCGAGCTCCCTGCTGCTCGAGCGAGACTCCTGCTGCTGAGCTTACATCT 3775
Qy 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3776 TCCCTCTCAGTCCAGTTCCGCTTCTGTGTACCGGATCATCACCCACACAGATGCTCG 3835
Qy 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
Db 3836 ACCACGTGTCTTGTTCATCATCTTCTTAACTGCATCACCATCGCATGGAGCGCCCA 3895
Qy 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
Db 3896 AAATTCACCCCAACAGCGCTGAACGATCTTCTGACCCCTCTCCAATTATCATCTTACCG 3955
Qy 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluG 1350
Db 3956 CAGTCTTCTGGCTGAATGACAGTGAAGTGTGGCACTGGGCTGGTGTCTTCTGGGAGC 4015
Qy 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
Db 4016 AGGCGTACCTGCGAGCAGTTGGAACGTGCTGGACGGGCTGTGGTGTCTCATCTCCGTCA 4075
Qy 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
Db 4076 TCGACATCTTGGTGTCTCATGCTCTCTGACAGCGGACCAAGATCTCTGGGCTGCTGAGGG 4135
Qy 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4136 TGCTCGGCTGCTCGGAGCCCTGCGCCGCTCAGGGTGTATCAGCGGGCGCAGGGGCTGA 4195

Qy 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
Db 4196 AGCTGGTGGTGGAGACGCTGATGTCCTCACTGAAACCCATCGGCAACATTGTAGTCATCT 4255
Qy 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
Db 4256 GCTGTGCTCTTCTCATCTTTCCGCATCTTGGGGGTGCAGCTCTTCAAAAGGGAAGTTT 4315
Qy 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlas 1470
Db 4316 TCGTGTCCAGGGCGAGATACCAAGAACATCACCAATAATCGAGCTGTGCCAGGCCA 4375
Qy 1470 erTyrArgTTPValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4376 GTTACCGGTGGTCCGCGCAAGTACAACTTTTGACAACTTGGCCAGGCCCTGATGTCCC 4435
Qy 1490 euPheValLeuAlaSerLysAspGlyTTPValAspIleMetTyrAspGlyLeuAspAlav 1510
Db 4436 TGTTCGTTTTGGCTCCAGGATGGTTGGGTGGACATCATGTACGATGGGCTGGATGCTG 4495
Qy 1510 alGlyValAspGlnGlnProIleMetAsnHisAsnProTTPMetLeuLysTyrPheIles 1530
Db 4496 TGGCGGTGGACACGACCCCATCATGAACACCAACCCCTGGATGCTGCTGTACTTCACT 4555
Qy 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
Db 4556 CGTTCCTGCTCATTTGTGGCTTCTTTGTCCTGAACATGTTTGGGTGTGGTGGAGA 4615
Qy 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysA 1570
Db 4616 ACTTCCAAAGTGTGGCAGCACCCAGGAGGAGGAGGCCCGCGCGGGAGGAGAAGC 4675
Qy 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4676 GCCTACGAAGACTGGAGAAAGAGAGAGGAATCTAATGCTGGAGCATGTAAATTGCTTCCG 4735
Qy 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 4736 GCAGCTCAGCCAGCGCTGCTGAGAGCCAGTGCAGAACCTTACTCTCCGACTACTCCC 4795
Qy 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG 1619
Db 4796 GCTTCCGGCTCCTGCTCCACCACTTGTGCACACGCACTACTTGGACCTCTTCAACAG 4855
Qy 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
Db 4856 GTGTATCGGGCTGAACGTGTGTCACCATGGCCATGGAGCACTACCAAGCCCCAGATTC 4915
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 4916 TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCACTTTTGTCTTGGAGTCAG 4975
Qy 1659 alPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTTPAsnGlnLeuA 1679
Db 4976 TTTTCAAACCTTGGTGGCTTCCGTTCCGTTCTTCCAGGACAGGTGGAACAGCTGG 5035
Qy 1679 splLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5036 ACCTGGCCATGTGCTGCTGTCCATCATGGGCATCACGCTGGAGGAATCGAGGTCAACG 5095
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5096 CCTGCTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTGCGCATTTGCCCGAG 5155
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5156 TGTCTGAAGCTGCTCAAGATGCTGTGGGCATGCGGGCGCTGTCGACACGCTGATGCAGG 5215
Qy 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
Db 5216 CCCTGCCCCAGGTGGGAACTCTCTTTCATGTGTGTGTGTTCATCTTTGTCAG 5275
Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779

Db 5276 CTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCC 5335
Qy 1779 euGlyArgHisAlaIleThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
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Qy 1799 erThrGlyAspAsnTTPAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5396 CCACAGGTGCATTTGGATGGCATTTATGAAGACACCCCTCCGGGACTGTGACCAAGAGT 5455
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5456 CCACCTGCTACAAACACGCTCATCTCGCTATCTACTTGTGTCTTCTGCTGTCAGCGCC 5515
Qy 1839 lnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
Db 5516 AGTTCGTGTAGTCAACAGTGTGATCGCGTGTGTATGAAGCACCTGGAGGAGAGCAACA 5575
Qy 1859 ysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuS 1879
Db 5576 AGAGGCCAAGAGGAGGCCGAGCTAGAGGCTGAGGCTGGAGCTGGAGATGAAGACCTCA 5635
Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTTPProGlyValGluGlyValA 1899
Db 5636 GCCCCAGCCCACTCGCCACTGGCAGCCCTTCTCTGGCTGGGTGAGGGCCCCG 5695
Qy 1899 snSerThrAspSerProLysProGlyValAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
Db 5696 ACAGCCCCGACACACCCCAACCTTGGGGCTCTGCACCCAGCGGCCACGCGAGATCAACCT 5755
Qy 1919 erGlyPheSerLeuGluHisProThr----- 1927
Db 5756 CCCACTTTTCCCTGGAGCACCCCAACGACGAGCGAGCTGTTTGACACCATATCCCTGCTGA 5815
Qy 1927 ----- 1927
Db 5816 TCCAGGGCTCCTCGAGTGGAGCTGAAGCTGTAGGACGAGCTGGCAGGCCAGGGGGCC 5875
Qy 1927 ----- 1927
Db 5876 AGCCCTCTGCTTCCCTTCTGCCCCAGCGCTGGAGGCTCCGACCCACAGATCCCTCTAG 5935
Qy 1927 ----- 1927
Db 5936 CTGAGATGGAGGCTCTGTCTCTGACGTACAGAGATTGTGTCTGAACCGTCTGCTCTAG 5995
Qy 1927 ----- 1927
Db 5996 CTCTGAGGATGACTCTTTGCTGTATGACATGCACACACTCTTACTTTAGTGCCCTGGAGA 6055
Qy 1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuThrV 1946
Db 6056 GCAATATGACGCCCCACCCACGAGCTGCCA-----GGACCAAGACTTACTGACTG 6106
Qy 1946 alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TGGGGAAGTCTGGGTCAGCCGAACGCACTCTGTGCCANTGACAGCTACATGTGTGCGC 6166
Qy 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnS 1986
Db 6167 ATGGGAGCACTGCGGAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCAAAGCTCAGT 6226
Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
Db 6227 CAGGCTCCGCTTGTCTCGTTCACTCCGACGACAGATACAGCTACATCTCGAGGCTTC 6286
Qy 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTTPGlyAlaIleProL 2026
Db 6287 CCAAAGATGACCTCATCTGTCTCAGCCCCACAGCCCCCACTGGGGGACCATCCCCA 6346
Qy 2026 ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046

Db 362 ATGACTTCATCTTTGCTCTTTGCCGTGGAGATGGTGGTGAAGATGGTGGCTTGGGCA 421
Qy 173 lePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAGTGTACTCTGGAGACACTTGGAAACCGGCTTGACTTTTTCATCTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGAGTCTGGAGTACTCGCTGCACTGCAAGACGTCAGCTTCTCAGTGTGAGGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTCGGACCGCTCAGGCGCAATTAACCGGGTGCACAGATCGCATCTTG 601
Qy 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCAGTGTGCTGTGGATACGCTGCCATGTGGGCAACGTCCTGCTGCTTCTGCTTCTG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTTCATCTTCGGCATCGTGGCTGCCAGCTGTGGCAGGCGCTCTTCGGAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTrpGlnT 293
Db 722 GCTTCTTACCTGAGAATTTTCAGCCTCCCTGAGCTGGACCTGGAGCGCTATTACCA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACGCGGAGAACGGCATGCGGT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAGCGTGCCCAACGCTGCGCGGGACGGGGGGTGGCCACTTGGCGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
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Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGGCATCACTTGGACAACTTG 1021
Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
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Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
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Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrPheSerGluT 433
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Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
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Qy 473 alTyrIleLeuArgGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
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Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
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Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
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Qy 533 ishHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
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Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
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Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
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Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
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Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
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Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCGGCGCCCTACAGCTCCATGCACAGCTGCTGGAGACACAGATA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
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Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGTCCAGACAGCTGCCCTTCTGTGCCCGCGCGGCGGAGGAGGTGGAGTGG 2041
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Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
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Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
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Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
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Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
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Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
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Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
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Qy 853 rpGluIleValGlyGlnGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 873
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Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
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Db 2759 TGCACACGAGGAGCTGAACAAAGTCTCTCAATGCTATGGCTTCCAGTCTGCTCTGGG 2818
QY 973 laAlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuL 993
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QY 993 aIAlaIleLeuValGluGlyPheGlnAlaGlu----- 1003
Db 2879 TGGCCATTCTGGTGGAGGGCTTCCAGCGGAGGAAATCAGCAAAACGGGAGATGCGAGTG 2938
QY 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTTAAGCTGATTACGTCCTGTCGACTCCAGCGGGGAGATGCCAACAGTCCG 2998
QY 1010 luSerGluProAspPheSerProSerValAspGlyAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGACCGGATTTCTTCTACCCAGCCTGATGCTGATGGGACAGGAAGTGTCT 3058
QY 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuL 1050
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QY 1070 luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGCGCTGGGCGCTGCTGCTGCGCGCACCCAGCAGCAGCGGTCGCGCAGAGCCTGGGGCG 3238
QY 1090 laHisHisGluMetLysCysProSerAlaArgSerProHisSerProTrpSerA 1110
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QY 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL 1130
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QY 1130 euLysArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGluGlyGlnGluS 1150
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QY 1150 erGlnAspGluGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
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QY 1170 rGHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGGTCCCTGGAGCGGAGGCAAGATTTCTTTGACCTTGCAGACACACACTGC 3535
QY 1190 lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
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QY 1210 ySAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCATGGCAAGTCCGGCTTCAGGGCGCTGGCCCGGCGCTGCGGCTGATGACCCCCAC 3655
QY 1230 euAspGlyAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgGileGlnAlaTr 1250

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Db 3716 GGATCCGAGCCGCACTCCCTGCTGCTCGAGCGAGACTCTCTGGTTCAGCTACATCT 3775
QY 1270 heProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
Db 3776 TCCCTCTCAGTCCAGGTTCCGCTTCTGTGTACCGGATCATCACCACCAAGATGTTTCG 3835
QY 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
Db 3836 ACCACGTGGTCTTGTTCATCATCTTCTTAACCTGATCACCATCCCATGGAGCGCCCA 3895
QY 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrrIlePheThrA 1330
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QY 1330 laValPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrrCysPheGlyGluG 1350
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QY 1350 lnAlaTyrrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
Db 4016 AGCGGTACTCTGGAGCAGTTGGAACGTGCTGCAACGGCTGTTGGTGTCTCATCTCCGTCA 4075
QY 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
Db 4076 TCGACATTTCTGGTGTTCATCTGCTGACAGCGGACCAAGATCTCTGGGCATCTGAGGG 4135
QY 1390 aIleuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
Db 4136 TGCTCGGCTGCTGGGACCTGCGCCGCTCAGGGTGTACAGCGGGCGCAGGGGCTGA 4195
QY 1410 ysLeuValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValIleC 1430
Db 4196 AGCTGGTGGTGGAGCGCTGATGCTCCTCACTGAACCCATCGCAACATGTTAGTCTCATCT 4255
QY 1430 ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
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QY 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
Db 4316 TCGTGTGCCAGCGCGAGGATACAGGAACATCACCAATAAATCGGACTGTGCGGAGGCCA 4375
QY 1470 erTyrrArgTrpValArgHisLysTyrrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
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Db 4496 TGGCGGTGGACGACGACCCCATCATGAACCAACACCCCTGGATGCTGTGTTACTTCTCT 4555
QY 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
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QY 1550 snPheHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysA 1570
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QY 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4676 GCCTACGAAGACTGGAGAAAAAGAGAGAAATCTAATGTGCGACGATGTAATTGCTTCCG 4735
QY 1580 ---SerLysGlnLysGlnMetAlaGluAlaGlnCysLysProTyrrTyrrSerAspTyrrSerA 1599

Db 4736 GCAGCTCAGCAGCGCTGCGTCAGAGCCCGAGTCAGAAACCTTACTACTCCGACTACTCC 4795
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Qy 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
Db 4856 GTGTCACTCGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACACAGCAGCCCCAGATT 4915
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Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
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Qy 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS 1919
Db 5696 ACAGCCCCGACAGCCCCAAGCCTGGGCTCTGCAACCCAGCGGCCCCAGCGAGATCAGCCT 5755
Qy 1919 erGlyPheSerLeuGluHisProThr----- 1927
Db 5756 CCCACTTTTCCCTGGAGCACCCCAAGCAGGACGAGCTGTTTGACACCATATCCCTGCTGA 5815
Qy 1927 ----- 1927
Db 5816 TCCAGGGCTCCTCGAGTGGAGCTGAAGCTGTGATGGAGCTGGCAGGCGCCAGGGGGCC 5875

Qy 1927 ----- 1927
Db 5876 AGCCCTCTGCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCGGACCCACAGATCCCTCTAG 5935
Qy 1927 ----- 1927
Db 5936 CTGAGATGGAGGCTCTGCTCTCTGACGTCAGAGATTGTGTCTGAACCCGTCCTGCTCTCTAG 5995
Qy 1927 ----- 1927
Db 5996 CTCTGACGGATGACTCTTTGCCCTGATGACATGACACACACTCTTACTTAGTGCCCTGGAGA 6055
Qy 1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV 1946
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Qy 1946 alArgIysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TGGGAAAGTCTGGGGTCAGCCGAACGCACTCTCTGCCCCAATGACAGCTACATGTGTCCGC 6166
Qy 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnS 1986
Db 6167 ATGGGAGCACTGCGGAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCAAAAGCTCAGT 6226
Qy 1986 erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
Db 6227 CAGGCTCCGTCCTGTCGTTCACTCCAGGCAGCAGATACACGCTACATCTTCGAGCTTC 6286
Qy 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL 2026
Db 6287 CCAAAGATGACCTCATCTGCTCCAGCCCCACAGCGCCCCCAACCTGGGGCAGCACATCCCA 6346
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Qy 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV 2066
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Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluG 2145
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Qy 2145 luProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCysArgA 2165
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Db 6767 GCCGGCTCTAGCTCTGCTGGATGACGACGAGGAGACACTCTATCGCCCTGCTGCTGCTGG 6826
Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG 2205
Db 6827 ACAGGGCTCCCAACCCCACTGGGCACAGACCCCTCTAACTTGGGGGCCGAGCTCTTG 6886
Qy 2205 lyGlyProGlySerArgProLysLysLeuSerProProSerIleSerIleAspProp 2225
Db 6887 GGGGGCTTGGGAGCCCGCCCAAGAAAAAATCGACCCCGCTGTATATCACCATAGACCCC 6946

QY 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlap 2245
 Db 6947 CCGAGAGCCCAAGGTCTCTCGACCCCGCCCGCCCTGGTATCTGCCCTCCGAGAGGGCTC 7006
 QY 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265
 Db 7007 CGTCCAGCGACTCCAAGGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCCTGC 7066
 QY 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA 2285
 Db 7067 CCTCCCAAGAAAGATGTGTGAGTCTCTCCGGTTTATCTCTGACCCAGACACCTGG 7126
 QY 2285 spPro 2286
 Db 7127 ACCCC 7131

Search completed: April 28, 2005, 09:29:50
 Job time : 2269 secs

QY	23	SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla	42	QY	382	allThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	491	CCGGATCGCCCGGGCCCCGGCTGGCCAGAGATGGACGAGGAGGATGAGCGGGCG	550	Db	1571	TCATCAGCTGGAGGGCTGGGTGCACATCATGTACTTTGTGATGATGCTCATCTCT	1630
QY	43	ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly	62	QY	402	YrAsnPhelIleTyrPheIleLeuLeuIleValGlySerPhePheMetIleAsnLeuC	422
Db	551	CCGAGAGTCCGGACACCCCGGAGCTTCATCGCGCTCAACGACCTGTGGGGGCGGGG	610	Db	1631	ACAATTTTCATCTACTTCATCTCATCTCATCTCGTGGGCTCTTCTTCATGATCAACCTGT	1690
QY	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG	82	QY	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	611	GCCGGCCGGGGCCGGGGTTCAGCAGAAAGAGACCCGGGACGGGACTCCGAGGGCGAGG	670	Db	1691	GCCTGGTGGTGAATTCGCCACGAGTTCTCAGAGACAAGAGCAGCGGAAGCCAGCTGATGC	1750
QY	82	lyLeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgP	102	QY	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	671	GGCTGCGGTACCGCGGCTGGCCCGCTGTTCTTCTTACTTGAGCCAGGACAGCGGCC	730	Db	1751	GGGAGCAGCGTGGGGTTCCTGTCCAAAGCCAGCACCTCGGTAGCTTCTCTCAGCCGC	1810
QY	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	122	QY	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgA	482
Db	731	CCGGAGCTGGTGTCTCCGACCGGTCTGAACCCCTGGTTTGAGCCGATCAGCATGTTGG	790	Db	1811	GCAGCTGCTATGAGAGAGTCTCAAGTACTCTGGTGTATCATCTTCGTAAGCAGCCCGCA	1870
QY	122	allIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142	QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	791	TCATCTTCTCACTGGTGACCTCGGCATGTTCCGGCCATGCGAGGACATCGCCTGTG	850	Db	1871	GGCTGGCTCAGGTCTCTCGGGCAGCAGTGTGCGGTTGGGCTGCTCAGCAGCCAGCAC	1930
QY	142	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaV	162	QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	851	ACTCCAGCGCTCCCGGATCTCTCAGCGCTTTGATGACTTCATCTTGTGCTTCTTTGGCG	910	Db	1931	CCCTCGGGGGCCAGGAGACCCAGCCAGCAGCAGCTGCTCTCGTCCCCAGCGCGCTAT	1990
QY	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA	182	QY	522	erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis	542
Db	911	TGAGATGGTGGTGAAGATGGTGGCTTGGGCACTTTGGGAAAAGTGTACTCTGGGAG	970	Db	1991	CGGTCCACCATCTGTGTGCACACCAACCAACCAACCAACCAACCAACCAACCAACCA	2050
QY	182	spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA	202	QY	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySera	562
Db	971	ACACTTGAACCGGCTTGACTTTTTCATCTCATCGCAGCGATGCTGGAGTACTCGCTGG	1030	Db	2051	GAACCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGACAGGGATGCCAATGGTCCC	2110
QY	202	spLeuGlnAnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222	QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1031	ACCTGCAGAACGTGAGCTTCTCAGCTGTTCAGGACGTCCCGTGTGTCGACCGCTCAGG	1090	Db	2111	GCAGGCTCATGTGTCACACACCTCGAGCGCTGCGCTCTCGGGGGCCCCCTGTGGCG	2170
QY	222	laIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM	242	QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisHisLeuGluProValArgCysGlnA	602
Db	1091	CCATTACCGGGTCCCGCAGATCGGCATCTTGTTCAGTGTGCTGTGATACGCTGCCCA	1150	Db	2171	CAGAGTGTGTGCACAGCTTCTACCATGCCAGTCCGACTAGCAGCAGTCCGCTGCCAGG	2230
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Db	1151	TGCTGGGCAACGTCCTGCTGCTGCTTCTGCTTCTGCTTCTTCTTCTTCTGCGCATCGTGGCG	1210	Db	2231	CGCCCCCTCCAGGTCCTCATCTGAGGCATCTCGGAGCATCTGGGCGACGCGGGAAGTGT	2290
QY	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheserLeuP	282	QY	622	yrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluV	642
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QY	282	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI	302	QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	1271	CCCTGAGCGTGGACCTGGAGCGCTATTACACAGACAGAAACGAGGATGAGAGCCCTTCA	1330	Db	2351	TGCTGCCAGCTCTGGGCCCCCAACCTCACCAGCTCAACATCCACCGGGGCTTACA	2410
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Db	1331	TCTGCTCCACGCCACGGAGAACGCGATGCGGTCTTCGAGAAGCGTCCCGCAGCTGGCG	1390	Db	2411	GCTCCATGCACAAAGCTGTGGAGACACAGATACAGGTGCTGCCAAAGCTCTTGCAGA	2470
QY	322	lyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerA	342	QY	682	leSerSerProCysSerLysAlaAspSerGlyValaCysGlyProAspSerCysProTyrC	702
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QY	342	snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyLysHisnP	362	QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspS	722
Db	1451	ACACCACGTGTCAACTGGAAACCACTACTACACCAACTGTCTCAGCGGGGAGCACAAAC	1510	Db	2531	GTGCCCGGGGGGCGGAGGAGGTGAGCTCGCCGACCGTGAATGCTGCTGCTGCTGCTG	2590
QY	362	roPheLysGlyAlaIleAsnPheserPheGlyTyrAlaTrpIleAlaIlePheGlnV	382	QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis	742
Db	1511	CTTCAAGGGGCCCACTCACTTGCACACATGCTGCTATGCTGCTGCTGCTGCTGCTGCTG	1570	Db	2591	GCAGGAGCTTATGATGTTACACAGGATGCCAGCAGCAGCAGCTCCCGGACCCACCA	2650
QY				QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762

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RESULT 2
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

Alignment Scores:
Pred. No.: 0 Length: 6822
Score: 10948.50 Matches: 2111
Percent Similarity: 94.03% Conservative: 32
Best Local Similarity: 92.63% Mismatches: 105
Query Match: 91.03% Indels: 31
DB: 3 Gaps: 5

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Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGlyLysAspP 73
Db 62 GGCTCAACGACCTGTCCGGGGGCGGGGGCGGGCGGGGGGGTCCAGCAGAAAGGACC 121
Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
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Qy 93 hePheThrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
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Db 1382 GGGTTGGGCTGTACAGACCCAGCACCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441
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Db 1682 GCCACITAGACCCAGTCCGTCGCCAGCGCCCCCTCCAGGTCCTCCATCTGAGGCATCC 1741
Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGGACTGTGGCAGCGGAGGTATCCCAACCGTGCACACCAAGCCCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
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Db 1982 CTTGTGTCAGACAGCTGCCCTACTGTGCCCGGGCGGAGGAGTGGAGTGGCTCG 2041
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RESULT 3

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US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859
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Alignment Scores:

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Pred. No.: 0 Length: 7405
Score: 10739.00 Matches: 2077
Percent Similarity: 92.09% Conservative: 29
Best Local Similarity: 90.82% Mismatches: 95
Query Match: 89.28% Indels: 86
DB: 4 Gaps: 5
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US-09-611-257A-24 (1-2287) x US-09-949-016-3859 (1-7405)

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QY      43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
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QY      63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
Db      461 GCCGCGCGGGGCGGGGTCAGCAGAAAGACCCCGGCGAGCGCGGACTCCGAGGGCGGAG 520
QY      82 lyLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
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QY      102 roArgSerTrpCysLeuArgThrValCysAsnPro---TrpPheGluArgValSerMetL 121
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QY      141 ysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheA 161
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QY 1241 euSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgG 1261
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QY 1301 ysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheL 1321
DB 4175 GCATCACCATCGCCATGAGCGGCCCAAAATTGACCCCAAGCGCTGAAACGATCTTCC 4234
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QY 1401 rgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuL 1421
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Qy 530 His 549
Db 1812 CATCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1871
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Db 2148 -----GGGAAGTGGCGCGGTGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2189
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Qy 668 LeuGluThrGlnSerThrGlyAlaCys-----HisSerSer-----Cys 680
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QY	1540	LeuAsnMet-PheValIcglyValValValGluaenPheHisLysCySArgGlnHIsGlnGlu	1559
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QY	1660	PheLysLeuValAlaAPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuasp	1679
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DB	5484	CTCCCCAGGTGGGAACCTTGGGCTCTTTTCATGCTCCTGTGTGTATCTATGTGTGG	5543
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DB	5724	AAGCACTCCCTGAGCTACCTCCCGCCCTGTCCGCCGTCTACTTCGTGACACTTCGTCTG	5783
QY	1837	ThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGlu	1856
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RESULT 5
US-09-398-522-51
; Sequence 51, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE REFERENCE: JHUI590
; CURRENT APPLICATION NUMBER: US/09/398,522
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
; NAME/KEY: CDS
; LOCATION: (373)...(3993)
US-09-398-522-51

Alignment Scores:
Pred. No.: 0 Length: 3993
Score: 6103.00 Matches: 1173
Percent Similarity: 95.49% Conservative: 12
Best Local Similarity: 94.52% Mismatches: 52
Query Match: 50.74% Indels: 4
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-398-522-51 (1-3993)
Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
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Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGCGCGCGCTGGCCAGAGGATGGACGAGGAGGAGGATGGAGCGGCG 400
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
Db 401 CCGAGGAGTGGGACACCCCGCGAGGCTTCTAGCGGCTCAACGACCTGTTCGGGGGCGCGG 460

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QY 82 LysLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
DB 521 GGTGCGCGTACCGGGCGCTGGCCCGGTGGTCTTCTTACTTTGAGCCAGGACGCCGCC 580
QY 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
DB 581 CGCGAGCTGGTGTCTCCGACGGTCTGTAAACCCCTGGTTGAGCGCATCAGCATGTTGG 640
QY 122 alileLeuLeuAnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
DB 641 TCATCCTCTCAACTCGTGGTACCCCTGGCATGTTCGGGCATGCGAGGACATCGCCTGTG 700
QY 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaV 162
DB 701 ACTCCAGCGGTGCCGGATCCTGCAGGCCCTTTGATGACTTTCATCTTGGCTTTTGGCG 760
QY 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
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QY 182 spThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
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QY 202 spLeuGlnAnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
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QY 482 rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA 502
DB 1721 GCCTGGCTCAGTCTCTTCGGCAGCAGGTGTGGGTGGCTGTCTCAGCAGCCAGCAC 1780
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QY 522 erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 542
DB 1841 CCGTCCACACCTGGTGCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 1900
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Db 3038 GCAAGTTTGGCTCTGACCGGATGGGACACCTTGCAGACCGGACCGAAGATTTTGACTCCT 3097
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Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT 982
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RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-BEG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-1 (1-6816)

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Qy 26 ProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGAGCCCGG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGGCGCTGAGGAGGCTCTGGATGGAGCT----- 326
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Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CAGAGCTGGCGCTATTCCTTCTGCTGCGACAGACCACCGCCCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGATCATCAAGATGGTGTGCAACCGCTGGTTGATGTGTAGCATGCTGGTGTCTCTGCTG 464

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 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
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 1836 LeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGlu 1855
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 5349 GCCCATGGCCCTGGCCCTGGCCGAGGCTGCTACCGGCTCC-----ProGly 2237

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 5531 CTTCCACCACTACTCTCTCGCCTCGCGCTGCAAGAGTGTCA-----CCA 5575
 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
 5576 CGACAA-----GCAAGAGGTGCAGCTGGCTGAGACGGA 5608
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 5609 GGCCTTCTCCCTGAACTCAGACAGGTCTCTGCTCATCTCTGGGTGAGCAGCTAGTCT 5668
 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
 5669 CGAGGA-----CCCCACAGCCCTG 5686
 2019 ProThrTrpGlyAlaIleProLys----- 2026
 5687 CCCACCTGG-----CCGCAAGGACAGCAAGGTGAGCTGGACCCACCTGAGCCCAT 5737
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 5738 GCGTGTGGAGACCTGGGCGAATGTTCTTCCCTTGT--CTCTACGGCGCTCGCCGG 5796
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 5797 ATCCAGAGAACTTCTGT--GTGAGATGGAGAGATCCAT-----TCAACC 5841
 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerIle 2085
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 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
 5914 -----CTCTCTGCCCATGCGCCGAGTCTTCCACCCCTG 5949
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 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
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 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSer 2219
 6119 CGCGGCGAGCTCAGACACACGCTCGAGGACAGCTGACCTGAGCGGACAGCCCGCGG 6178
 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237

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Db 6218 CGGCTGTGCGCGCGCGCTGCGCGCGCGCTGCGCGCGCGCGCTTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGCGGCGCGCATAGCGCAGCAGCGGCGGCTCCAGCAGCCCGGCTG 6337

RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCICUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

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Query Match: 45.06% Indels: 413
DB: 4 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)
Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCTCCTCATCTGCAGCAGCGCCAGCGCTGAGCGAGTCCACCGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGCGCTGAGGAGCTCTGGATGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTy 85
Db 327 -----GATCCT-----CATGTCCACAC 344
Qy 86 ProAlaLeuAlaProValValPhePheTyLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACTGGCGCTATTGCTTCTTCTGCTGCGACAGACACCACCGCCCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCCCGTGTGATGTGTACATGCTGGTATCTCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspLeuAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACACGCGCTGGCGACGACATGGACTGCTCGACCGC 524

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Qy 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetVal 165
Db 525 TGCAGATCTCGAGGCTTTGATGACTTTCATCTTTATCTTTTGGCATGGAGTGTG 584
Qy 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyLeuGlyAspThrTrpAsn 185
Db 585 CTCAAGATGTGGCCCTGGGATTTTGGCAAGAAGTGTACCTCGGGGACACATGGAAC 644
Qy 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTySerLeuAspLeuGlnAsn 205
Db 645 CGCTGGATTCTTCATCGTCGAGGAGGATGTCGAGTACTCCCTGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaLeuAsnArg 225
Db 705 ATCAACCTGTAGCATCCCGACCGTGGCGCTCTGAGGCCCTCAAGACCATCAACCGC 764
Qy 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGCGGATCCTGGTGAACCTGCTCTCGACACACTGCCCATGCTGGGAAT 824
Qy 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCTGTCTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluLeuAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGCGCTGTGCGTAACCGCTGCTCTCGAGAGAACTTCACCATCAAGGGAGTGTG 944
Qy 286 AspLeuGluProTyTrpGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGCCCCCATACTACACGCGGAGGAGATGATGAGATGCCCTTCACTGCTCCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
Db 1005 TCGGCGCACAATGGGATAATGGGCTGCATGAGATCCCGCGCTCAAGAGCAGC----- 1058
Qy 326 GlyGlyProProCysSerLeu-----AspTyTrpGluThrTyTrpAsnSer 339
Db 1059 ---GGCGTGAGTGCTGCTGCTGCCAGGACGAGCTTACGACTTTGGGGGGGGCGGCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyTrpThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGCTCTGTGTCACTGGAAACCGTTACTACATGTGTGCGGCAGC 1175
Qy 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyAlaTrpIle 377
Db 1176 GGCAGCGCCCAACCCCAACAGGCGTCCATCAACTTTGACAAACATCGGTTATGCTTGAT 1235
Qy 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyTrpPheValMetAsp 397
Db 1236 GTCATCTTCAGGTGATCACTCTGGAGGCTGGGTGGAGATCATGTACGTATGAT 1295
Qy 398 AlaHisSerPheTyTrpAsnPheIleTyTrpPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCACTCTCTTACAACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTCTTC 1355
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCGCTCGTGTGTATAGCGACCGCTTCTCGGAGACCAAGCAACGGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheIleuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGTGATGTGGAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1472
Qy 458 PheSerGluProGlySerCysTyTrpGluGluLeuLysTyTrpValTyTrpIleLeuArg 477
Db 1473 TAGCGCGAGCTGGCGACTGCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTCGCG 1532
Qy 478 LysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCGCTGGCGCTCTACCGAGCGCTGCGAG 1574

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3276	TCGGTGCAGCTGGCGGAGCTGGTCCCGCGGTGGGGCCGCCACACCCCGGGCGCGCTGGAGG	3333
1202	SetSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
3336	CGGCGAGCGCGGCGCCCGCGGCATGAGGACTGCAATGGCAGGATGCCACG-----ATC	3389
1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
3390	GCCAAAGACGTCTTTCACCAAGATGGGCGACCGCGGGATCGCGGGAGGATGAGGAGAA	3449
1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
3450	ATCCAGTACACCTGCTGCTCCGCGGTCCGCAAGATGATCAGCTCTATAAGCCCGACTGG	3509
1259	CysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeu	1278
3510	TGCAGGTCGCGGAAGACTGGTGTCTACTCTCTCTCTCCCGAGAACAGTTCCGGGTC	3569
1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIlePhe	1298
3570	CTGTGTGACAGCATTATTGGCCCAAAACTCTTCGACTACGTCGTCTCTGGCTTCATCTTT	3629
1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
3630	CTCAACTGTCATCACCATCGCCCTGGAGCGGCTCAGATCGAGCGCGCAGCCGACACG	3689
1319	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
3690	ATCTTTCTACCGTGTCCAACTACATCTTCAGGCCATCTTCGTGGCGGAGATGACATTG	3749
1339	LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358
3750	AAGGTAGTCTCGCTGGGCGCTGTACTTCGGCGAGCAGCGCTACCTACGACGACGTGGAAC	3809
1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
3810	GTGCTGATGGCTTTCTTGTGCTTCGTGTCAATCATGACATCGGTGGTGTCCCTGGGCTCA	3869
1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
3870	GCCGGGGAGCCAGATCTTGGGGGTCTCCGAGTCTTGGCGTCTTCGCGCACCTTACGC	3929
1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
3930	CCCCTGCTGTGCATCAGCGCGGCGCGGCTGAAGCTGTGTGGTGGAGACACTCATCTCC	3989
1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438
3990	TCCCTCAAGCCCATCGGCACATCGTGCTCATCTGCTGTGCTCTTCTTCATCATCTTTGGC	4049
1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
4050	ATCTGGAGTGCAGCTCTTCAAGGCAAGTTTACCACACTGTCTGGGCGTGGACACCCGC	4109
1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
4110	AACATCACCAACCGCTCGGACTGCATGCGCGCCAACCTACCGTGGTCCATCACAATAC	4169
1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
4170	AAC TTCACAACCTTGGGCGCAGGCTCTGATGTGCCCTCTTGTCTCTGGCATCCAAAGGATGGT	4229
1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIleMet	1518
4230	TGGGTGAACATCATGTAAATGAGTGGATGCTGTCTGTGGACACGAGCTGTGACC	4289
1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
4290	AACCACAAACCCCTGGATGCTGTACTTCATCTCTCTCTGTCTCATCGTCAGCTCTTTT	4349
1539	ValLeuAsnMetPheValGlyValValAlaGluAsnPheHisLysCysArgGlnHisGln	1558
4350	GTGCTCAACATGTTGTGGGTGTCTGGTGGAGAACTTCACAAGTCCCGGACGACACAG	4409

Qy	1559	GluGluGluAlaAArgArGdgluLuLyAArgLeuAArgLeuGluLyLysAArg	1578
Db	4410	GAGCGTGAAGAGGCACGGCGCGCTGAGAGAAGCGGTGCGGCCCTGGAGAAGAACGCC	4469
Qy	1579	ArgSerLySGluLySGlnMetAlaGluaAlaGlnCysLySProTyTYrSerAspTYrSer	1598
Db	4470	CGG-----AAGGCCCAAGCGCGTCGCCCTACTATGCACCATATTGT	4508
Qy	1599	ArgPheArgLeuLeuValHisLeuLysThrSerHisTYrLeuAspLeuPheIleThr	1618
Db	4509	CACACCGGCTGCTCATCACTCCATGTCGACAGCACCTACTCTGGACATCTTCATCACC	4568
Qy	1619	GlyValIleGlyLeuAenValValThrMetAlaMetGluHisTYrGlnGlnProGlnIle	1638
Db	4569	TTCATCATCTGCCCTCAACGTGGTGACCATGTCCCTGGAGCACTACAATCAGCCCACGCTCC	4628
Qy	1639	LeuAspGluAlaLeuLySileCysAenTYrIlePheThrValIlePheValPheGluSer	1658
Db	4629	CTGGAGACACCCCTCAAGTACTCCAATAATATGTTCCACCACTGTCTTTGTCTGGAGGCT	4688
Qy	1659	ValPheLySLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsnGlnLeu	1678
Db	4689	GTGCTGAAGCTGTGGCATTTGGTCTGAGAGCGCTCTTCAAGAGCCATGGAACACGCTG	4748
Qy	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTGTGCTACTGTCTCAGTCATCGGCATCACCCCTGGAGGAGATCGAGATCAAT	4808
Qy	1699	LeuSerLeuProIleAenProThrIleIleAArgIleMetArgValLeuArgIleAlaAArg	1718
Db	4809	CGCGCCCTGCCCATCAATCCACCANTCATCCGATCATAGAGGTTCCTGCGCATTTGCCCGA	4868
Qy	1719	ValLeuLySLeuLeuLySmetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln	1738
Db	4869	GTGCTGAAGCTGTTGAAGATGGCCACAGGAATCGGCCCTCTGTGGACACGTTGGTGCAA	4928
Qy	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPheIlePheAla	1758
Db	4929	GCITTTGCCCCAGGTGGCAACCTGGGCCCTCTCTTCATGTGCTCTTCTTTCATCTATGCT	4988
Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTCGGGTGAGGCTCTTTTGGGAAGCTGTCTGCAACGACGAGAACCCGCTGCGAGGCG	5048
Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATAGCGCGGATGCCACCTTCGAAACCTTCGGCATGGCCCTCTCTCACACTCTTCCAGGTC	5108
Qy	1799	SerThrGlyAspAsnTrpAsnGlyIleMetLyAspProSerArgAspCys---AspGln	1817
Db	5109	TCCACGGGTGACAACTGGAACGGGATCATGAAGACACCGTGGGGACTGCACCCACGAC	5168
Qy	1818	GluSerThrCysTYrAsnThrVal-----IleSerProIleTYrPheValSerPheVal	1835
Db	5169	GAGCGCAGCTGCTCGAGCAGCTTCGATTTGTGTGCGCGCTGTACTTCGTGAGCTTCGTG	5228
Qy	1836	LeuThrAlaGlnPheValLeuValAenValValIleAlaValLeuMetLySHisLeuGlu	1855
Db	5229	CTACCGCGCAGTTGCGTCTCATCAACGTGGTGGCTGTGTCTCATGAAGACACTTGGAC	5288
Qy	1856	GluSerAsnLySGluAlaLySGluAlaGluLeuGluAlaGluLeuGluLeuGluMet	1875
Db	5289	GACAGCAACAGGAGGCGCAGGAGGACGCCGAGATGGATGCCGAGCTTCGAGCTGGAGATG	5348
Qy	1876	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly	1894
Db	5349	GCCCATGGCTGGGCCCTGGCCCGAGGCTGCCTACCGGCTCC-----	5390
Qy	1895	ValGluGlyValAanSerThrAspSerProLySProGlyAlaProHisThrThrAlaHis	1914
Db	5391	-----CCGGCGCCCCCTGGCCGAGGGCGCG--	5414

QY 1915 IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro----- 1930
 Db 5415 ---GGAGGGGGCGGGCGG- GGCGACACCGAGGGCGCTTGTCCGGCGGTGCTACTC 5470
 QY 1931 -----HisProGluGluValPro 1938
 Db 5471 GCGTGGCCAGGACTCCTGGAGGGGAGCTGACCATCATCGACAACCTGTCGGGTCCAT 5530
 QY 1939 LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
 Db 5531 CTTCCACCACTACTCTCGCTCGCGCTGCAAGAGTGCA-----CCA 5575
 QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
 Db 5576 CGACAA-----GCAAGAGGTGCGAGCTGGCTGGAGCGGA 5608
 QY 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
 Db 5609 GGCCTTCTCCCTGAACCTCAGACAGGTCCTCGTCCATCCTGCTGGGTGACGACCTGAGTCT 5668
 QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
 Db 5669 CGAGGA-----CCCCACACGCTG 5686
 QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
 Db 5687 CCACACTGG-----CCGCAAGACGACGAGGTGAGCTGGACCCACCTGAGCCCAT 5737
 QY 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla 2045
 Db 5738 GCGTGTGGGAGACTGGCGAATGCTTCTCCCTTGT-CCTCTACGGCGCTGCGCGG 5796
 QY 2046 IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGlu 2065
 Db 5797 ATCCAGAGAACTTCTCTGT---GTGAGATGGAGGATCCCAT-----TCAACC 5841
 QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheThrPglyGlySerIle 2085
 Db 5842 CTGTCCGCTCTGGCTGAACATGACA----- 5868
 QY 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
 Db 5869 -----GCAGTCAAGCACCCCAAGTCCCTTCT 5895
 QY 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
 Db 5896 CCC-----CGATGCTCCACG- 5913
 QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
 Db 5914 -----CTCTCTGCCATGCGCAGCGAGTCTTCCACCCCTG 5949
 QY 2146 ProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSerCys 2163
 Db 5950 CAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGCACTGGCACTGGAACCCCTCCCAAGA 6009
 QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCys 2183
 Db 6010 TTGGCTG-CAGGCTCTCTGGCATCT-----CTGGGTACCAAGGGTCACTGT 6059
 QY 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
 Db 6060 ACCCTCTCCGGCAGGCCACCGGAGGACACAGCTGCTGGACGCCAGCCCGCAGCAG-CTC 6118
 QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSer 2219
 Db 6119 CGCGGGCAGCGTCGAGACCACTGCTGAGGACAGCTGACCTGACCGTGGAGCAGCCCGCGG 6178
 QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
 Db 6179 -----TGCCCTGGGGCCCGCCGCTGCTCCAGGACCCCGGC 6217
 QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257

Db 6218 CGGCTGTCCCGCGCTCCCGCGCTGCGCGCTGCGCGCTTCTTTCAGCCT 6277
 QY 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
 Db 6278 GCGGGGGTGGGGGCGCATCAGCGCAGCCACAGCAGCGGGGCTCCACACGCCCGGGCTG 6337

RESULT 8
 US-09-404-650-3
 ; Sequence 3, Application US/09404650
 ; Patent No. 6309858
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/09/404,650
 ; CURRENT FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 6855
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (192)..(6755)
 ; US-09-404-650-3

Alignment Scores:
 Pred. No.: 0 Length: 6855
 Score: 5420.00 Matches: 1228
 Percent Similarity: 61.97% Conservative: 235
 Best Local Similarity: 52.04% Mismatches: 500
 Query Match: 45.06% Indels: 402
 DB: 63 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-404-650-3 (1-6855)

QY 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
 Db 207 TCCCGCGCTCTCTATCTGACAGCCCGCTGAGCGAGGAGTACACGAGGAGCAG 266
 QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
 Db 267 CCGGACCCCG- 278
 QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
 Db 279 -----AGCCCCCATCTCTCCCGCGCGCTGGAGGAGCTCTGGATGGAGCT- 326
 QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
 Db 327 -----GATCCT-----CATGTCCACAC 344
 QY 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
 Db 345 CCAGACCTGGCGCTATTGCTCTTCTGCTGCGACACACACACAGCCCGGAACTGG 404
 QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
 Db 405 TGCAATCAAGATGGTGTGCAACCCGTTGTAATGTGTGATGCTGTGTGATCTCTGCTG 464
 QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
 Db 465 AACTGTGTACACTTGGCATGTACACCGCTGGACGACATGAGTGCCTGTCCGACCGC 524
 QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
 Db 525 TGCAAGATCTGCGAGGCTTTGATGACTTTCATCTTTATCTTTTCTTTCATGGAGTGGT 584
 QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185

QY	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPhePhePheSerIle	914	QY	1220	AlaArgThrLeuArgThrAsp	---AspProGlnLeuAspGlyAspAspAspGlu	1238
Db	2361	ATGGACAACGTCGCCACCTTCGTCATGCTGCTCTTCACTTCTTCACTTCTGAGCATC	2420	Db	3390	GCCAAAGACGTCCTTCAACAGATGGCGGATCGCGGAGGATGAGGAGAA	3449	
QY	915	LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp	933	QY	1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258	
Db	2421	CTTGGGATGATATTTTGGCTGCAAGTTTCAGCTCCGACGACACTGGAGACACGGTG	2480	Db	3450	ATCGACTACACCTGCTGCTTCCGCGTCGCAAGATGATCGACGCTCTATAAGCCGACGTGG	3509	
QY	934	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	953	QY	1259	CysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeu	1278	
Db	2481	CCGACAGGAAGAACTTCGACTCCCTGCTGTGGGCGATCGTCACTGTGTTCAGATCCTC	2540	Db	3510	TGCAGGTCGCGCAAGACTGTGCTACCTTCTTCTCCGAGAACAGGTTCGGGTC	3569	
QY	954	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerTrpAla	973	QY	1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298	
Db	2541	ACCAGAGAGACTGGAAAGCTGCTTCTACATGATGGATGGCTCCACITCTCCCTGGGCC	2600	Db	3570	CTGTGTGAGACCATATTTGCCCAAACTCTTCGACTACGTCTGCTCTGCTTCTCATCTTT	3629	
QY	974	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	993	QY	1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318	
Db	2601	TCCCTCTACTTTTCGCCCTCATGACCTTCGGCAACTATGTGCTCTTCAACCTGCTGGTG	2660	Db	3630	CTCAACTGCATCACATCGCCCTGGAGCGGCTCAGATCGAGCGCGGACGACCGAACGC	3689	
QY	994	AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro	1013	QY	1319	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338	
Db	2661	GCCATCTGTGGAGGCTTCCAGGCGGAGGTGACGCCAATCGCTTCTACTCGGACGAG	2720	Db	3690	ATCTTTCTCACCGTGTCCAACTACTTTCACGGCCACTTTCGTTGGGCGGAGATGACATG	3749	
QY	1014	AspPhePheSerProSerVal	1023	QY	1339	LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358	
Db	2721	GACAGAGCTCACTCAACATAGAGAGTTTGATAAGCTCCAGGAAGCGCTGGACAGC	2780	Db	3750	AAGTAGTCTCGCTGGGCTGTACTTCGGCGAGCAGCGCTACCTACGACGAGCTGAAC	3809	
QY	1024	GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys	1043	QY	1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378	
Db	2781	GGAGATCCCAAG-----CTCTGCCCAATCCCATGACCCCAATGGGACCTGGACCCC	2834	Db	3810	GTGCTGGATGGCTTCTTGTCTTGTGTCATCATCGACATCGTGGTGTCTTCCGCTCA	3869	
QY	1044	SerLeuLeuProLeuIleIleHisThr-----AlaAlaThrProMetSer	1059	QY	1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398	
Db	2835	AGTCTC-----CCACTGGGTGGGCACCTAGTCTCTGCTGGGCTGGCGACCTGCC---	2885	Db	3870	GCCGGGGAGGCAAGACTTTCGGGGTCTCCGAGTCTTTCGGGCTCTTCGCGCACCTACGC	3929	
QY	1060	HisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr	1079	QY	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluLeuMetSer	1418	
Db	2886	-----CCCCGACTCTCACTGACGCGGACCCCATGCTGTGGTGGCTCCCGGAGAGC	2942	Db	3930	CCCTCGCTGTCTATCAGCGCGCGCGCGCTGAGCTGGTGGTGGAGACACTCACTCC	3989	
QY	1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer	1099	QY	1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438	
Db	2943	AGTGCATGCTCTA-----GGGAGATGAGCTATGACACGCTCCCTGTCACG	2993	Db	3990	TCCCTCAAGCCCATCGGCNACATCGTGTCTATCTGTCTGTCTTCTCATCATCTTGGC	4049	
QY	1100	AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119	QY	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlnGluAspThrArg	1458	
Db	2994	TCCCGAGCTCTACTACGGGCCATGGGGCGGACGCGGCTGGGCGGCGGCTCGCTCC	3053	Db	4050	ATCTGGGAGTGCAGCTTCAAGGGCAAGTTTCTACCACTGTCTGGGCGTGACACCCGC	4109	
QY	1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg	1139	QY	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478	
Db	3054	AGCTGGAAC-----AGCTCAAGCAAGACCGCCGCTGGCGGAGCAT	3095	Db	4110	AACATCACCAACCGCTCGGACTGCATGGCCGCCAATACCTACCGCTGGGTCCATCACAATAC	4169	
QY	1140	ArgSerLeuLeuSerGlyGlu-----GlyGlnGlnSerGlnAspGluGluSerGlu	1158	QY	1479	AsnAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysLysGly	1498	
Db	3096	GAGTCCCTCTCTCTCGGAGCGCGCGCGCGCGCGCGCTGCGAGGTTGCGCGGAC	3155	Db	4170	AACCTCGACAACTGGCGGAGCTCTGTATGTCCTTGTCTGTCATCCTCAAGGATGT	4229	
QY	1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----AGCTCAAGCAAGACCGCCGCTGGCGGAGCAT	3195	QY	1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518	
Db	3156	GAGGGCG	3215	Db	4230	TGGGTGAACATCATGTATCAATGAGCTGATGTCCTTGTCTGTCGACGAGCTGTGACC	4289	
QY	1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181	QY	1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538	
Db	3216	CCCCATCTGGGACCGCGCACCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	3275	Db	4350	GTGCTCAACATGTTGTGGGTGTCTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	4399	
QY	1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201	QY	1559	GluGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg	1578	
Db	3276	TCGGTGGACCTGGCGGAGCTGGTGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG	3335	Db	4410	GAGCTGAAGAGGACCG	4469	
QY	1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219	QY	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598	
Db	3336	CGCGGCG	3389					

Db 1578 ---CGGCCGACGCCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCCGAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGCGCCCGCCCAACCTGGGCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACAGCTGTCGCCGCAACATAGCCCTCGATGCG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGGTGAC-----CCCATCCCGCCACGCTGGCTCC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
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Db 1818 GGCTCC-----GGGAGCTCGCTGGTGGCGAGGACGAGGCG----- 1853
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Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
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6314 CCTCGGGGGTGGCGGCGCATCAGCGACGACAGCGGGGGCTCCACAGCCCGG 6373
Db

Qy 2277 Leu 2277
Db 6374 CTG 6376

RESULT 10

US-09-404-650-12
; Sequence 12, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-404-650-12

Alignment Scores:

Pred. No.:	0	Length:	6503
Score:	5407.00	Matches:	1234
Percent Similarity:	61.05%	Conservative:	241
Best Local Similarity:	51.08%	Mismatches:	502
Query Match:	44.95%	Indels:	444
DB:	3	Gaps:	60

US-09-611-257A-24 (1-2287) x US-09-404-650-12 (1-6503)

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Qy 23 SerAspPro-----ProGlyProArgLeuAlaArgGlyTrpThrArgArg 38
Db 115 GCTGATCCCGGAATCCGAGGCGTGGGGCGCGGG--GCGCGGGTCTCTCCACGCGG 173
Qy 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla 51
Db 174 CTTGGGGACACCGGTCAACCCCGGTCTCTGCGGGAGCAGCCCGCTGCCGGCCACG 233
Qy 52 -----SerArgSerSerThrTh 57
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Dbb
Qy
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266 laGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuLeuProLeuSerValA 286
954 CAGCGCTGCTACGGAACCGCTGCTCTCTGGAAGAAGAACTTCCACATAACAAGGGATGCG 1013
286 spLeuGluProTyTrTyTrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306
1014 CCCTGCCCCCTTATTACCAACGAGAGAGATGACGAGATGCCCTTTATCTGCTCCCTGA 1073
306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGlyG 326
1074 CTGGGGACAATGGCATCATGGCTGCCACGAGATCCCCCCCACCTGAAGAGCAG----- 1126
326 lyGlyProProCysSerLeu-----AspTyrGluThrTyTrAsnSerS 340
1127 --GCCCGGAATGCTGCCTGTCCAAGATGATGTATGATGATCTCGGGCGGGCGGCCAGG 1184
340 erSerAsnThrThr----CysValAsnTrpAsnGlnTyTrThrAsnCysSerAlag 358
1185 ACCTCAAGCCAGCGGTCTGTGCGCTCAACTGGAACCGCTACTCAACGCTGTCCGCGCAGG 1244
358 lyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyTrAlaTrpIleA 378
1245 GCAACGCCAACCTCACAGGGCGCCATCAACTTTTGACAACATTGGCTATGCTCGCGGATTG 1304
378 laIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyTrPheValMetAspA 398
1305 TGATTTTCCAGGTGATCACTCTGAAGGCTGGGTGGAGATCATGTACTGTGTATGTGACG 1364
398 laHisSerPheTyTrAsnPheIleTyTrPheIleLeuLeuIleValGlySerPhePheM 418
1365 CACATTCTTTCTACAACCTTCACTTCACTTCTGTGCTCATCATAGTGGGCTCTCTTCTCA 1424
418 etIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
1425 TGATCAACTTGTGCTGTGTGCATGACACCCAGTCTCTGAGACCAAGCAACGCGGAGC 1484
438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
1485 ACCGGCTGATGCTGGAGCAACGCCAGCGCTACCTGTCC--TCCAGCACGGTGGCCAGTT 1541
458 heSerGluProGlySerCysTyTrGluLeuLeuLysTyTrLeuValTyTrIleLeuArgL 478
1542 ACGCTGAGCCGGTGATGTGTATGAGAGATCTTCCAATATGTCTGCATCATCTCTCGCA 1601
478 ysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeus 498
1602 AAGCAACGGC-----CGTGCCCTAGGCCTCTACGAGCCCTG--- 1639
498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
1640 -----CAGA 1643

[illegible]

Qy	870	ArgLeuMetArgValLeuLysValArgPheLeuValArgGlnLeuVal	899
Db	2339	CGGTTGCTGGGGTGCCTAAAGCTGGTGCCTTCATGCGCGCGTGC	2398
Qy	890	ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle	909
Db	2399	GTGCTCATGAAGACCATGGCAACGTGGCCACCTTCATGCAATGCTACTCATCTGTTGTTATC	2458
Qy	910	PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp	929
Db	2459	TTCATCTTCAGCATCCTTGGGATGCATATCTTTGGCTGCATAATTCAGCCTCCGACGGAC	2518
Qy	930	---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr	948
Db	2519	ACGGGAGACACCGCTTCCTGCAGGAAGAACTTCGATTCTTACTGTGGGCATCGTCACA	2578
Qy	949	ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTrpAsnGlyMetAlaSer	968
Db	2579	GTGTTCCAGATCCCTACTCAGGAGACTGGAACGTTCTCTGTACATGATGCGCTCC	2638
Qy	969	ThrSerSerTrpAlaAlaLeuTrpPheIleAlaLeuMetThrPheGlyAsnTrpValLeu	988
Db	2639	ACCACCCCTGGGCTCCCTCTATTGTGGCTCATGACCTTGGCACTACGTTCTC	2698
Qy	989	PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys	1008
Db	2699	TTCATCTCTGTTGGCTATCTCTGGTAGAGGTTTCAGGCTGAGGCTGATGCTAATCGT	2758
Qy	1009	SerGluSerGluProAspPhePheSerProSerValAspGly	1022
Db	2759	TCCTGCTCTGATGAGGACGAGCTCAATTTGGAGGAGTTTGACAAAGTCCCGACG	2818
Qy	1023	-----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu	1040
Db	2819	GGCCTGCACACAGTAGAGATCTCAAGCTCTGCCAATACCCATGCACCCATGGACAC	2878
Qy	1041	LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet	1058
Db	2879	CTGACCTCAGCCTC-----CCTCTGGGTGGCATCTGGGCTCTGCTGTAGCATGGGT	2932
Qy	1059	SerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg	1078
Db	2933	ACTGCCCCCGCCCTCTCACTGCAGCCAGACCCGGTACTGTGTGGCCCTPAGACTCTCGAAA	2992
Qy	1079	ThrSerSerSerGlySerAlaGluProGlyValAlaAlaHisGluMetLysCysProPro	1098
Db	2993	AGCAGTGTATGTCCTCTG-----GGCAGATGAGCTATGATCATCAGCATCTTGTCTCC	3043
Qy	1099	SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg	1118
Db	3044	AGTCCCGGAGCTCTACTACGGGCCCTTGGGGCGCAGTGGGACCTGGGCTAGCGCGCGC	3103
Qy	1119	SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgSerProSerGlyGlu	1138
Db	3104	TCCAGCTGGAAC-----AGCCTGAACACAAAGCGCCCTCAGCTGAG	3145
Qy	1139	ArgArgSerLeuLeuSerGlyGluGlnGluSer-----GlnAspGluGluGluSer	1156
Db	3146	CATGAGTCTTACTGTCTGGGAGGTGGAGGTAGCTGCTCAGGCGCTGTGAAGCGCC	3205
Qy	1157	SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3206	CGGGAGGAGGGCCCAACTCGCACCGCACCCCTGTGATGCTCCACACGGCACACCGCGCAC	3265
Qy	1170	-----ArgHisArgGlySerLeuGluArgGluAla	1179
Db	3266	CATGGACCCCACTGGCACACCGTCAACCGACACACCGCCGAGCTCTGTCTGTATACC	3325
Qy	1180	LysSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer	1199
Db	3326	AGGAGCTCTGTTGACCTGGGAGACTGGTCCCGCTGTGGTGCCCACTCACGGGCCGCT	3385
Qy	1200	-----GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly	1217

[illegible]

4460	Db	CACAGGAGGCTGAGGAGGCCGGAGGCGTGAGGAGAAACGGCTGCGCGCCCTGGAAAG	4519
1577	Qy	lysArgSerIysGluLysGlnMetAlaGluAlaGlnCysIysProTyrTyrSerAsp	1596
4520	Db	AAGCCCGT-----AAGCTCAGAGGCTGCCTACTATGCTACC	4558
1597	Qy	TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe	1616
4559	Db	TACTGTCCCAAGCGTCTCATCCACTCATGTGCACACGCCACTACCTGGACATCTTC	4618
1617	Qy	IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro	1636
4619	Db	ATTACCTTCATCATCTGCCCTCAATGTGTCAACATGTCCTCGGAGCACTCAACACGCT	4678
1637	Qy	GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe	1656
4679	Db	ACATCCCTAGAGCAGCGCTTAAGTACTGCAACTACATGTTCAACCATGCTCTTTGTGCTG	4738
1657	Qy	GluSerValPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTTPAsn	1676
4739	Db	GAGCTGTGCTGAAGCTGGTGGCATTTGGCTGAGGCGTTTCTTCAAGGACCGATGGAAC	4798
1677	Qy	GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGlu	1696
4799	Db	CAGCTGACCTGGCCATTTGTCTCTCTCCGTATGGGCATCACTCGGAGAGATCGAG	4858
1697	Qy	ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle	1716
4859	Db	ATCAATGCCGCCCTTCCCATCAACCCACCATCATCGGTATCATGCGTGTTCGCGTATC	4918
1717	Qy	AlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal	1736
4919	Db	GCCCGGTGTGAAGCTATTGAAGATGGCCACAGGAATGCGGCGCTGCTGGACACAGTG	4978
1737	Qy	MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle	1756
4979	Db	GTACAGCTCTGCCCCAGGTGGGCAACCTGGCGCTGCTCTTCATGCTGCTCTTCTTCATC	5038
1757	Qy	PheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys	1776
5039	Db	TATGCTGCTCTGGGAGTGGAGCTCTTCGGAAGCTGTGTGCAATGACGAGAACCCTGT	5098
1777	Qy	GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe	1796
5099	Db	GAGGCGATGAGCGGCACGCCACCTTTGAAACCTTCGCGCATGGCTTCCTCACGCTCTTC	5158
1797	Qy	ArgValSerThrGlyAspAsnThrPAsnGlyIleMetLysAspProSerArgAspCys---	1815
5159	Db	CAGCTCTCCACAGCGGTAATCTGGAATGGAAATATGAAGGACACCCCTGCAGACTGTACC	5218
1816	Qy	AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer	1833
5219	Db	CATGATGAGCGCACGTGCTTAAGCAGCGCTGCAGTTGTGTACCGCTCTACTTTGTGAGC	5278
1834	Qy	PheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHis	1853
5279	Db	TTGCTGCTCACAGCTCAGTTCTCGTCTCATCAACGTGTGTGGCGGTGCTGATGAACAT	5338
1854	Qy	LeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeu	1873
5339	Db	CTGATGACAGCAACAAGGAGGCCACGAGGAGATGAGATGGATGTGTGATGTGAGCTG	5398
1874	Qy	GluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	1893
5399	Db	GAGATG-----	5404
1894	Qy	GlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAla	1913
5405	Db	---GCCCATGGCTCGGCCCTCGCCCTGGCCCTCGCTGGT-----	5443
1914	Qy	HisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGlu	1933
5444	Db	-----CCTGCCCCCTGC	5455

Qy	1934	GluValProValPro	---LeuGlyProAspLeuLeuThrVal	-----	1944
Db	5456	CCCTGCCCTCCCTCGCTGTGTGCGCCGAGCTCCACCTAGTTTCACCTGGGGCTCCGGGG	5515		
Qy	1947	ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn	1966		
Db	5516	CGAGATCGGAGGGGCGAGTGTCTGGAGGC---GACACCGAGAGTCACTGTGTCCCGCAC	5572		
Qy	1967	---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGln	1985		
Db	5573	TGCTATTCTCCAGCCAGGAGACCTG---TGG	5608		
Qy	1986	SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu	2005		
Db	5609	AGCGTCTCTTAAATCATCAAGGACTCTTGGAGGGGAGCTGACCATCATTTGACAACTG	5668		
Qy	2006	ProLysAspVal---HisTyrLeuLeuGlnProHisGlyAla	2018		
Db	5669	TCITGGTCCGTCTTCCACCACTACGCCTCACCTACGGCTGTGGCAAGTGTCAACATGAC	5728		
Qy	2019	-----ProThrTrpGlyAlaIleProLysLeuProProPro	2030		
Db	5729	AAGCAAGAGACAGTCTTCAATCCATCTGTGTGGGGATGACCTGAGTCTTGTAGGACCCCA	5788		
Qy	2031	GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer	2050		
Db	5789	CGGCTGCCACAGGGCCCCAAGAGAGCAGAGGTGAACTAGAGCTCCGGAGCCCATGC	5848		
Qy	2051	LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu	2068		
Db	5849	AGGCTGGAGACCTGGATGAATGCTTTGGGCCCTTGCCAAGCGAGCGAGTGTCCACAGCG	5908		
Qy	2069	ProSerProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGln	2088		
Db	5909	CCAGAGAG-CCTGCTGTGCCAGAT-----GGGGGCCATTCCATTCAACC-CTG	5954		
Qy	2089	GlnArgSerGlyIleGlnSerLysValSerLysHisIleArg	2102		
Db	5955	TCCAGTCTTGCTCAACACAGAGAGCAGCAACCCAGAGCCCTTCTCCCGCGATG	6014		
Qy	2103	-----LeuProAla	2105		
Db	6015	GCTCCAGCCCTCTCTGTAGATGCCTGCTGAGTTCTTCCACCTGTGTGTCTGCCAGCC	6074		
Qy	2106	-----ProCysProGly	2112		
Db	6075	AGAAGGGGAGGAACCGGGCATGAGTGCAGGAACCTTGCCCAAG-ATTGCATCTCAGGG	6133		
Qy	2113	SerTrpAlaLys---AspProGluThrArgSerSerLeuGluLeuAspThrGluLeu	2131		
Db	6134	TCCTGGGCATCGGTGAGTCAACGAGTGTCAACTGCACCCCTCTTGGCGCCAGGCTACTGTG	6193		
Qy	2132	SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluLeuProLeuPheProArgAsp	2151		
Db	6194	AGTGACAGCTCTTGGATGCCAGTCTTAGCAGTCA	6229		
Qy	2152	LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeu	2171		
Db	6229	-----	6229		
Qy	2172	AspGluGlnArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg	2191		
Db	6230	-----GCGGCAACCTTACAGACACACTGGAAAGACAGTCTGACT	6268		
Qy	2192	LeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro	2211		
Db	6269	CTGAGTGACAGTCCCCTGGCTGTCCCTGGGGCCCGCGGTCCAGTGTCTGGG	6322		
Qy	2212	LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg	2231		
Db	6323	CGGCTAGCTGTGTACCGGCAACCCCGGG-----CCGCTCAGCTCGCGGCGCGTGG	6376		

[illegible]

Db 5405 ---GCCATGCGCTCGGCCCTGCGCCCTGCGCCCTGCTGGT----- 5443
Qy 1914 HisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGlu 1933
Db 5444 -----CCCTGCGCCCTGC 5455
Qy 1934 GluValProValPro---LeuGlyProAspLeuLeuThrVal----- 1946
Db 5456 CCTGCGCCCTGCGCCCTGCTGCTGCGCGAGCTGCCACCTAGTTCACTGGGGCTCGCGGG 5515
Qy 1947 ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn 1966
Db 5516 CGAGGATCGGAGGCGAGTCTGAGGC---GACACCGAGAGTCACTGTGCGGCAC 5572
Qy 1967 ---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGln 1985
Db 5573 TGTATATCTCCAGCCAGGAGACCTG---TGG-----CTGGAC 5608
Qy 1986 SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu 2005
Db 5609 AGGTCTCTTTAATCATCAAGACTCTTGGAGGGGAGCTGACCATCATGACAACTG 5668
Qy 2006 ProLysAspVal---HisTyrLeuLeuGlnProHisGlyAla----- 2018
Db 5669 TCTGGGTCCGTCTTCCACCACTACGCTCACCTGACGGCTGTGGCAAGTGCACCATGAC 5728
Qy 2019 -----ProThrTyrGlyAlaIleProLysLeuProProPro 2030
Db 5729 AAGCAAGAGACAGGTCTTCATCATCTGCTGGGGATGACCTGAGTCTTGAGGACCCCA 5788
Qy 2031 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2050
Db 5789 CGGCTGCCACAGGCCCCAAGAGAGCAAGGTGAAGTACAGAGCTCCGGAGCCCATCG 5848
Qy 2051 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu-----ValSerGly 2068
Db 5849 AGGCTGGAGACCTGGATGAATGCTTTTGGCCCTTTGCCAAGCGAGCGAGTCCACAGCG 5908
Qy 2069 ProSerCysProLeuThrArgSerSerPheTyrGlySerSerIleGlnValGln 2088
Db 5909 CCAGAGAG---CTGCTCTGCGAGAT-----GGGGGCCATTTCATTAACC---CTG 5954
Qy 2089 GlnArgSerGlyIleGlnSerLysValSerLysHisIleArg----- 2102
Db 5955 TCCAGTCTGGCTCAACAG 6014
Qy 2103 -----LeuProAla 2105
Db 6015 GCTCCAGCCCTCTCCTGTAGTGTGCTGAGTTCTTCCACCTGCTGCTGCTGCCAGCC 6074
Qy 2106 -----ProCysProGly-----LeuGluPro 2112
Db 6075 AGAAGGGGAGGAGAACCGGCGATGAGTGCAGGAACCTCGCCCAAG-ATTGCACCTTCAGGG 6133
Qy 2113 SerTyrAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu 2131
Db 6134 TCTGGGCATCGTGAAGTACCGAGTCACTGACCTCTGCGCCAGGCTACTGTG 6193
Qy 2132 SerTyrIleSerGlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAsp 2151
Db 6194 AGTGACACGTCCTTGGATGCCAGTCTCCTAGCAGCTCA----- 6229
Qy 2152 LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgProGlyPheTyrLeu 2171
Db 6229 ----- 6229
Qy 2172 AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg 2191
Db 6230 -----CGCGGCGACCTACAGACCACTCGAAGACAGTCTGACT----- 6268
Qy 2192 LeuCysProSerProSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro 2211
Db 6269 CTGAGTGACAGTCCCCCGGCTGCGCTGGGCGCGCGCTCCAGGTCCAGTGCCTGGG-----CCA 6322

Qy 2212 LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231
Db 6323 CGGGTAGCTGTACCGCCACCCGCG-----CCGCTCAGCCTGCGGGCGCGTGG 6376
Qy 2232 ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247
Db 6377 CCTGTTTAGTCTGCGTGGGCGGCCCATCAGGTAGCCACAGAGTGGCGGCTCCAC 6436
Qy 2248 -----AspSerLysAspProSer 2253
Db 6437 CAGCCCTGGCTGCTCACTCCACGAGCTCCATGAGACCCCTCT 6476
RESULT 12
US-09-949-016-15601
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15601
Alignment Scores:
Pred. No.: 9,78e-114 Length: 70308
Score: 2055.00 Matches: 697
Percent Similarity: 21.05% Conservative: 35
Best Local Similarity: 20.04% Mismatches: 108
Query Match: 17.05% Indels: 2640
DB: 4 Gaps: 21
US-09-611-257A-24 (1-2287) x US-09-949-016-15601 (1-70308)
Qy 4 HisArg-----ValProArg-----CysValArgThrProProLeuArgGly 17
Db 9479 CACAGCATGATCGATTATTATCCCAATGGCTTGTGCAATAGTCAGGGTATTGTGGC 9538
Qy 18 SerAlaArgProSerSerAspProProGlyProArgLeuAlaArg-----GlyTyrThr 35
Db 9539 TTGTCTCTCTTACAGATGAGGAAGCTGGTCCAGAGGTGAGATGACCAAGGTGG--- 9595
Qy 36 ArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArgSer--- 54
Db 9596 -----GACTCCCTCTCTGTGATGAGGAGTCTG 9622
Qy 55 -----SerThrThrCysProGlyProGlyAlaAlaGlySerThr 69
Db 9623 GGGCTGGGGCTGGTCTGCGTGTATGTAGGGCCCTGGCACCACACCTGCT---TAGCCT 9679
Qy 70 GluLysAspProGly-----SerAlaAspSerGluAla 80
Db 9680 CAGATGGAGCCAGGAGGTAAACGAGGAGGTGTTAGGGCGGGTTCGGGGCGCGCCT 9739
Qy 81 GluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSer 100
Db 9740 CAGCTCCAGCTTGGCCAGCTGTTTCT----- 9766
Qy 101 ArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgValSerMet 120

Db	14121	TGCTCTGCTCAAGTTTTTAGCTCTCAGGACAAGTCCTGTAGAGAGGCGCATCCATCATAT	14180	Db	15201	GACACACATTGAGAGAGAGATTAAAGAAAGATTAAAGATCTACTCTAGGACCTAGGACTAG	15260
Qy	412	-----	412	Qy	412	-----	412
Db	14181	AGTAGAGGGACACCAGATGCAGAGTCAGAGGAAATCCAAGGTCAAGCGCGGACTTAAAC	14240	Db	15261	CTCCAGAGAGAGATGAAGACAAAATAAGGCAGCTCCTTGTGAGAGACAGAGGGTAGGCC	15320
Qy	412	-----	412	Qy	412	-----	412
Db	14241	TGCTATTGGGACCTTGGGCAAGTCATTCTCATGAGGCGCTCCAGACTGCTCTGGGCTC	14300	Db	15321	TGAGAAAGAGCAAGTCCCCAAGGCCACCTCATTCTGCTGCGTAACCTCCCTCGTGGG	15380
Qy	412	-----	412	Qy	412	-----	412
Db	14301	TGTTTCTCATGGTAAATGAATGGTTCTCAACTGAGATGATACCACCTCTCCAGAG	14360	Db	15381	AAGAGTGGCAGGCTTGGGGCGAAGCTGACTGAGGCGCTGTTCCCATCCCTCGGCCACCA	15440
Qy	412	-----	412	Qy	412	-----	412
Db	14361	GGCATTGGAAATGGGAAGGTGATTCTGTTTTGATTTTTTTTAATAGCTTTAATTGAG	14420	Db	15441	CCTCAAGGGTGAGGCCAGTGTCTCAGGGAAGTGGGTCTTCTCACCATGTGCCCCCCCC	15500
Qy	412	-----	412	Qy	412	-----	412
Db	14421	ACATAACTCACATATCATTCATTCATCCCTTTGAATGAATCCAGTGGTTTTTAAGCAT	14480	Db	15501	ACCCCCACTCCCTTCCCTCTGCGCTTGGGAGAGGGGAAGAGCAGACAGGGAGATA	15560
Qy	412	-----	412	Qy	412	-----	412
Db	14481	GTTTACAGAGTTCGTGTTTTTTTGTAAAGACAAGGGAGTGCAATTGGCAATTTGTTACTG	14540	Db	15561	AGGGCGCTAGTTTTCCACCCTCCACACACACCCCCCTGAAAAATCTTTCTTAACAGCTCTCTG	15620
Qy	412	-----	412	Qy	412	-----	412
Db	14541	GGGAGGGGAGAGAAGCTAAACATCTGAATGCTTGCAATAAAGAATTATTCTACCCA	14600	Db	15621	GAATCACACTAGTGAAGCTAATTATCATTAATTACTAGGACACGATCTAGAAAAAAAAT	15680
Qy	412	-----	412	Qy	412	-----	412
Db	14601	AAATTCTGATCAGTGATCAATTGGTGTAAATGCTGCTGATCTCTTATTCCTGCCAGTT	14660	Db	15681	CTGCTTTGTCAACCAATAATTCATTTTCCTTTCATTTGGGATTGTTGTCCAAGCAATGGCT	15740
Qy	412	-----	412	Qy	412	-----	412
Db	14661	CAGAAATGCCAGACTTTAAGAAGGCAGACGAGGCAAAAGCAGCAATTTAATAG	14720	Db	15741	GTTCCAGAGTCTTGGGAAACTGAGGCGTGGAGATGGGACTGGGTAGTGTGAGCAAGT	15800
Qy	412	-----	412	Qy	412	-----	412
Db	14721	TTTTAATCACTACCAITTCATAGTTAATAACTTTCATCGCCACCCTTTGAGCTAATATTA	14780	Db	15801	CAGGTGCGACGCTGACTAGTCTGTAGGGTCAAGGGTTCAGCCCCCTCCACATCTGAGGGA	15860
Qy	412	-----	412	Qy	412	-----	412
Db	14781	TTGAGCACTTACTATGCGCAGCCCTGATCTAAGACTTTCAATGTGCTGGTGCAITTA	14840	Db	15861	GGGGGCGACAGGGAATGGGACAGACAAGGCCAATGGTCCCTGTTTTCAGATGAGGAT	15920
Qy	412	-----	412	Qy	412	-----	412
Db	14841	ATCCTCACCGTGATCCTCCATTTTACAGATGAGGAAACTGACATTTCTCATTTATCT	14900	Db	15921	ATGAGGTCCCATGGCTAAGGTCTCTCGCCAAAAGTCACACAGCTAGAAATGGGGCTAGA	15980
Qy	412	-----	412	Qy	412	-----	412
Db	14901	GACCTACAGACGCTTTGCCATGCTGTATTAATCTCAAGAGTGGGCGCATCACTGC	14960	Db	15981	AGCAGAGTCTGTAAATGATGTTTTTGTCAAGATCTCAAGGCTCAATATAATTTGAAAA	16040
Qy	412	-----	412	Qy	412	-----	412
Db	14961	TGAGTATGTGTAACATCTGCTGCCTGTTTAATCTCGTCGTCCTCGTGAGGTGCCAG	15020	Db	16041	CCCCATGCTCAATATTGGTTCATTTCCACAGCATTCGCTACTCTTAATGGAAATTGC	16100
Qy	412	-----	412	Qy	412	-----	412
Db	15021	GGCAGGATTGTGTTCCCATCTCTTAATGAGAAATTCAGCGCCCCCAGAGGGTGGTCA	15080	Db	16101	GGAAGGGTCTGCGTCTCTGAGGTGCGTGTGTTAGGACAGGGAATTTGAGAGATTG	16160
Qy	412	-----	412	Qy	412	-----	412
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Qy	412	-----	412	Qy	412	-----	412
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Qy	412	-----	412	Qy	412	-----	412
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Db 62 GCGGTGGAGATGGTCAATCAAGATGGTGGCGCTGTGGCGCAGAAAGTGTACCTG 121
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Qy 201 LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 220
Db 182 TTGGACGGACACAACCTGAGCTCTCGGCTATCAGGACCGTGGCGGTCTGGCGCCCTC 241
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Db 1000 ----- 1000
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[illegible]

RESULT 14

US-08-455-543A-7
Sequence 7, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:

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 Db 5336 GGTCTGGGCTGAATACGACCCGCTGCGTGGCGCATCAGTTACATCAATGATGTTGA 5395
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 Db 5501 CATGACTGTTCATCAGTCCACGCTGATGCCCTCATCCGACGGCAGCTGGAGATCAA 5560
 QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
 Db 5561 GCTGCCCCAGCTGG-----GACAAGCAGCATCAGTGTGACCGGAGTTGAG 5608
 QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGly----- 1975
 Db 5609 GAAGGAGATTTCCGTTGT---GTGGGCCAATGTGCCCAAGAGACTTTGGACTTGTGCT 5665
 QY 1976 -----HisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1987
 Db 5666 ACCACCCCATAGCTGATGATGACATGAGTGGGAGGTTTATGACGCTCTGATGATATT 5725
 QY 1988 SerIleLeuSerVal-----HisSerGlnPro----- 1996
 Db 5726 TGACTTCTACAGCAGAACAAACACAGACAGATGCAGCAGGCTCTCTGGAGCCT 5785
 QY 1997 ---AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnPro 2015
 Db 5786 CTCCAGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5830
 QY 2016 HisGlyAlaProThrTrpGlyAlaIleProLysLeuPro----- 2028
 Db 5831 CTTGAGCAGACACAGCCGCTGTGCTCCGAGGAGCCCGGTTTCTTCGACAGAGAG 5890
 QY 2028 ----- 2028
 Db 5891 TTCCACCTCCTCAGCAATGGCGGGCCCATACAAACCAAGAGAGTGGATCAAGAGTC 5950
 QY 2029 -----ProProGly 2031
 Db 5951 TGTCTCTGGGCACTCAAAGACCCAGGATGCACCCATGAGCCGAGCCACCCCTGGA 6010
 QY 2032 ArgSerProLeu-AlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsp----- 2049
 Db 6011 GGTGGCCCATCCACAGATCCTCTGTGGGGCGTCTCAGGAGCAGCTGGCTGTGACCTTCA 6070
 QY 2050 -----SerLeuAspValGl 2054
 Db 6071 GATCAGAGCATAAACCCGAGGGGCTCTGATGGGAGCCCGACGCTGGGCTGGAGAGCCA 6130
 QY 2054 nGlyLeuGlySerArgGluAspLeuSerGluValSerGlyPro-----SerCy 2071
 Db 6131 GGGTCAGCGGCTCTCCATGCCCGCTTCCGCGCAGACTCAGCCGCTCAGAGATCCAG 6190
 QY 2071 sProLeuThrArgSerSerSerPheTrpGlyGlySerIleGlnValGlnIleArgse 2091
 Db 6191 CCCCATGAAGCCTCTCATCTCC-----ACGCTGGCCAGCGGCC 6229

Qy 2091 rGlyleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeu-- 2110
Db 6230 CCGTGG-GACTCACTTTGAGCAGCACCCCGGACCCCTAGCCAGCGCTCGT 6288
Qy 2111 ----GluProSerTrpAlaLysAspProGlu-ThrArgSerSerLeuGluLeuAspT 2129
Db 6289 CGCACCAACACACACCGCTGCCACCGCGCAGGAGCAGAGAGAGTCCCTGGAGA 6348
Qy 2129 hrGluLeuSerTrpIleSerGlyAspLeu-----LeuProSerSerGlnGluProL 2147
Db 6349 AGGGGCCAGC---CTGTCTGCCGATATGATGCGCAGCAGAGAGTGTGGGGCCGG 6405
Qy 2147 euPhePro-----ArgAspLeuLysCysTyrSerV 2158
Db 6406 GGCTGCCCGGGAGAGGGGCTACAGCTGCCGCGGGAACAGAGAGCGCGGAGGAGC 6465
Qy 2158 alGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGlnArgArgHis 2178
Db 6466 GGGCGCGGTCCAGAGAGCGGAGGAGCGCTCTCTCTCTCGGAGAGAGCGCTTC- 6524
Qy 2178 erIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSer 2197
Db 6525 -----TACTCTGCGACCGCTTTGGGGCGCTGAGCCCCCGAAGCCCAAGCCCTCC 6576
Qy 2197 ----- 2197
Db 6577 TCAGCAGCCACCAACCTGCCAAGCTGGCCAGAGCGGAGCCGCCACCCAGAGGCA 6636
Qy 2198 ----SerLeuGlyGlnProLeu-----G 2205
Db 6637 GTGGTTCGTAATGGAGGCGCTTGTGTCAACATCTGTGTAGCACCCCGCGCGCG 6696
Qy 2205 lyGlyProGlySerArgProLysLysLysLeuSerPro---ProSerIleSerIleAspP 2224
Db 6697 GTGGCGGAGGAGCTCCCGCAGAGCGCCCTGACTCCCGCCCGCAGCATCACTTACAAGA 6756
Qy 2224 roProGluSer-----GlnGlySerArgProCysSerP 2236
Db 6757 CGGCCAATCTTCACTTCCGCGGGCTGAGACGAGCTCCCTGCTTCTTCTCC 6816
Qy 2236 roGly-----ValCysLeuArgArgArgAlaProLas 2247
Db 6817 CAGCGCGCTCAGCGCTGGGCTTTCCGAACACACGCGCTGCTGAGAGAGACCCCTCA 6876
Qy 2247 erAsp-----SerLysAspProSerValSerSerProLeuA 2259
Db 6877 GCCAGCCCTTGGCCCTTGGCTCTCGAATGGCTGTGACCTTACCTGGGCGAGCGTCTGG 6936
Qy 2259 spSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeu----- 2274
Db 6937 ACAGTGAGGCTCTGTCCAGCGCTTGTGAGGAGACGCTCACTTTTCGAGAGGCTGTGG 6996

RESULT 15

US-08-193-078B-7

; Sequence 7, Application US/08193078B

; Patent No. 5846757

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

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; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; METHODS

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN

; STREET: 1660 UNION STREET

; CITY: SAN DIEGO
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,078B
; FILING DATE: 07-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,354
; FILING DATE: 10-APR-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53607
; TELEPHONE: 619-238-0999
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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163
; NAME/KEY: 5'UTR
; LOCATION: 1..143
; NAME/KEY: 3'UTR
; LOCATION: 7161..7362

US-08-193-078B-7

Alignment Scores:

Pred. No.: 2,92e-96 Length: 7362

Score: 1745.50 Matches: 662

Percent Similarity: 37.80% Conservative: 356

Best Local Similarity: 24.58% Mismatches: 879

Query Match: 14.51% Indels: 798

DB: 2 Gaps: 84

US-09-611-257A-24 (1-2287) x US-08-193-078B-7 (1-7362)

Qy 14 ProLeuArgGlySerAlaArgProSerSerAspProGlyProArgLeuAlaArgGly 33

Db 66 CCGCTCTGAGCGCTGCGCGCCCGCGCCCTCCCTGCGCGGGCGG---CTGGGCGGGGA 122

Qy 34 TrpThrArg-ArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerAr 53

Db 123 TGCACGCGGGCGCGGAGCATGTCTCGGGGACGAGCTGGGCGGCGCGCTATGGA 182

Qy 53 gSerSerThrThrCysProGlyProGlyAlaAlaGly---AlaGlySerThrGluLysAs 72

Db 183 GGCGCGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGT 242

Qy 72 pProGlySerAlaAspSerGluAlaGluGlyLeu----- 83

Db 243 CCAGGGGGGCTGC---AGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 299

Qy 84 -----ProTyrProAlaLeuAlaProVal----- 91

Db 300 GCGCGGACCATGCGGCTGTACAAC-CCATCCCGGTCAAGCAGAACTGCTTACCGCTCAA 358

Qy	92	----	ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrVa	110
Db	359	CCGCTCGCTCTCGTCTTCAGCGAGGACAACTCGTCCGAAATACCGAAGCGCATCAC	418	
Qy	110	lCysAsnProTrpPheGluArgValSerMetLeuValleLeuLeuAsnCysValThrLe	130	
Db	419	CGAGTGGCCCTCCATTCGAGATAATAGCTTCGGCCACCATCATCGCCAACTGCTGCTGCT	478	
Qy	130	uGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGl	150	
Db	479	GGCCCTG-----GAGCAGACCTCCCTGATGGGACAAACAGCCCATGTCCGA	526	
Qy	150	nAlaPheAspAsp-----PheIlePheAlaPhePheAlaValGluMetValValLy	167	
Db	527	CGCGCTGGACGACACGGAGCCCTATTTCATCGGGATCTTTTGTCTTCGAGCGAGGATCAA	586	
Qy	167	sMetValAlaLeuGly---llePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnAr	186	
Db	587	AATCATCGCTCTGGGCTTGCTTTCCAAAGGGCTCTTACCTGCGGAACGGCTGGAACGT	646	
Qy	186	gLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAspLe	203	
Db	647	CATGGACTTCTGTGTCTCTTCACAGGATGCTTTCGCCAGCGCTCGAACTGACTTCGACCT	706	
Qy	203	uGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIl	223	
Db	707	CGCA-----ACACTGAGGGCTGTGCGTGTGCTGAGGCCCTGAAGCTGGT	751	
Qy	223	eAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLe	243	
Db	752	GTCTGGGATTCCAAAGTTTGCAGGTGGTGTCTCAAGTCCATCATGAAGGCCATGGTTCCACT	811	
Qy	243	uGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGl	263	
Db	812	CTTCAGATTGGGCTGCTCTCTCTTTCGTCATCCTCATGTTTCCCATCATGTGGCCCTGGA	871	
Qy	263	nLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLe	283	
Db	872	GTTCTACATGGCAAGTTCCACAGGCTGTTC-----CCCAA	910	
Qy	283	uSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy	303	
Db	911	CAGCACAGATCGGAGCGCGCTG-----	932	
Qy	303	sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl	323	
Db	932	-----	932	
Qy	323	uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsnTh	343	
Db	933	-----GGTGACTTCCCTGTGCAGGAGGCCCCAGCCGGCTGTGCAGGGCGACAC	985	
Qy	343	rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPh	363	
Db	986	TGAGTGC-----CGGGAGTACTGGCCA-----GGACCCAA	1015	
Qy	363	eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIl	383	
Db	1016	CTTTGGCATCACCACACTTGACATAATCTCTTTGGCATCTTTCAGGGTGTTCAGTGCAT	1075	
Qy	383	eThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPheTy	402	
Db	1076	CACCATGGAGGGCTGGACTGACATCTCTATATACAAACGATCGCGCCGGCACACCTG	1135	
Qy	402	rAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCy	422	
Db	1136	GAACTGGCTCTACTCTCATCTCATCATCATCGGCTCTTCTTCTCATGCTCAACCTGGT	1195	
Qy	422	sLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer-----	438	
Db	1196	GCTTGGGCGTCTCTCGGGGAGTTTGCCAAAGGACGAGAGGGGTGGAGAACCGCGCGC	1255	

QY	439	-----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl	456
DB	1256	: : : : : CTTCCTGAAGCTGC CGCGCAGCAGCATCGAG-----	1289
QY	456	aSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLe	476
DB	1290	: : : : : -----CGAGAGCTCAACGGGTACTCTGGAGTGGATCTT	1321
QY	476	uArgLYeAlaAalaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLe	496
DB	1322	: : : : : CAAGCGGAGGAAGTCA TGTGCGCCAGGAGGAC-----	1355
QY	496	uLeuSerSerProValalaArgSerGlyGlnGluProGlnProSerGlySerCysThrAr	516
DB	1356	: : : : : -----AGGAATGCAGAGGAGAAGTCCCCTTTTGCGACTGCTGAAGAG	1396
QY	516	gSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHis	536
DB	1397	: : : : : AGCGGCCACCAGAAGACAGCAAGTAATCACTGTATCCAC-----	1433
QY	536	sTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspAr	556
DB	1434	: : : : : -----GCAGAGGAGGAGAGACCG	1453
QY	556	gAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGl	576
DB	1454	: : : : : GTTTGCAGAT-----	1463
QY	576	yGlyProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGl	596
DB	1463	-----	1463
QY	596	uProValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrVa	616
DB	1463	-----	1463
QY	616	lGlySerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAs	636
DB	1463	-----	1463
QY	636	pLysAlaLeuValGluValalaProSerProGlyProProThrLeuThrSerPheAsnIl	656
DB	1463	-----	1463
QY	656	eProProGlyProPheSerSerMethisLysLeuLeuGluThrGlnSerThrGlyAlaCy	676
DB	1463	-----	1463
QY	676	sHisSerSerCysLyaleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPr	696
DB	1464	: : : : : -----CTCTGTGCTGTGGATCCCCCTTCGCGCGCGCAGC-----	1499
QY	696	oAspSerCysProTyrCysAlaargThrGlyAlaGlyGluProGluSerAlaAspHisVa	716
DB	1500	: : : : : -----CTCAAGAGCGGGAAGACAGAGAGCTCGTCACTACTT	1534
QY	716	lMetProAspSerAspSerGluAlavalTyrGluPheThrGlnAspAlaGlnHisSerAs	736
DB	1535	C-----	1535
QY	736	pLeuArgAspProHissErArgArgGlnArgSerLeuGlyProAspAlaGluProSe	756
DB	1536	: : : : : -----CGGAGGAAGGAGAAG-----	1550
QY	756	rSerValLeuAlaPheTrpArgLeulleCysaspThrPheArgLysIleValAspSerLy	776
DB	1551	: : : : : -----ATGTTCCGGTTTTTT-----ATCCGCGCATGCTGAAGGCTCA	1588
QY	776	sTyrPheGlyArgGlyLeMetileAlaIleLeuValAsnThrLeuSerMetGlyIleGl	796
DB	1589	GAGCTTCTACTGGGTGCTGTGTGTGGCCCTGAACAACACTGTGTGTGCCCATGTG	1648
QY	796	uTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheTh	816

Db 1649 GCATTACACAGCGCGGCTTACACAGACCTGTATTTTGCAGAGTTTGTTCCT 1708
Qy 816 rSerLeuPheAlaLeuGluMetLeuLeuLeuValTyGlyProPheGlyTyr11 836
Db 1709 GGGTCTCTTCTCACAGAGATGTCCTCAAGATATATGGCTGGGGCCCAAGACTACTT 1768
Qy 836 eLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrpGluIleVa 856
Db 1769 CCGGTCTCTTCACTTCTGACTTGTGGGTCTATCTGGGAGCGCTCTTTGAGTGGT 1828
Qy 856 lGlyGln-----GlnGlyGlyLeuSerValLeuArgThrPheArgLe 871
Db 1829 CTGGCGGCCATCAAGCGGGAAGCTCTTTGGGATCAGTGTGCTGGCGGCTCTCGCCT 1888
Qy 871 uMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValle 891
Db 1889 GCTGAGGATCTCAAGACTCAAGTACTGAGCTCTCTCGGAACTCTGGTGTCTCCT 1948
Qy 891 uMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe11 911
Db 1949 GCTGAATCTCATGAAGTCCATCATCAGCTGCTCTTCTCTCTCTCTCTCTCTCTCTCTCT 2008
Qy 911 ePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAs 931
Db 2009 CTTGCGCCTCTGGGATGAGCTGTTGGGGACAGTTCAACTTCCAGGATGAGACTCC 2068
Qy 931 pThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheG1 951
Db 2069 CACA-----ACCAACTTCGACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 2116
Qy 951 nIleLeuThrClnGluAspTrpAsnLysValLeuTyrAsnGlyMet----- 966
Db 2117 GATCCTGACGGGAGAGACTGGAATGATGATATACAGGGATCGAATCGCAAGGCGG 2176
Qy 967 -AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTy 986
Db 2177 CGTCAGCAAGGCGATGTCCT 2236
Qy 986 rValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAl 1006
Db 2237 CACTCTGCTGAATGCTTCTTGGCCATCGCTGTGGACAACCTGGCCAACGCCCAAGAGCT 2296
Qy 1006 aThrLysSerGluSerGluProAsp----- 1014
Db 2297 GACCAAGATGAGAGGAGATGGAAGAGCAGCAATCAGAAAGCTTGTCTGTGAAAAGGC 2356
Qy 1015 -----Phe-PheSerProSerValAspGlyA 1023
Db 2357 CAAGAAGTGGCTGAAGTCAGCCCATGCTGCGCGCAACATCTCCATGCGCGCCAGGCA 2416
Qy 1023 spGlyAspArgLysLysArg-LeuAlaLeuValAlaLeuGlyGluHisAla----- 1039
Db 2417 GCAGAACTCGGCCAAGGCGCTCGGTGGGAGCAGCGGCGCCAGCAGCTACGGCTGCA 2476
Qy 1040 -----GluLeuArgLysSerLeuLeu-----ProProLeu 1049
Db 2477 GAACCTCGGCGCCAGCTGCGAGCGCTGTACAGCGAGATGACCCCGAGGAGCGGCTGCG 2536
Qy 1050 IleIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGly 1069
Db 2537 CTTGCGCACTACGCGCCACTGCGGCGCGCATGAAGACGACCTGGACCGCGCTGGT 2596
Qy 1070 GluAla-LeuGlySerGlySerArgThrSerSerSerGlySerAlaGluProGlyAl 1089
Db 2597 GGTGAGCTGGCGCGCAGCGCGCGGGGCCGCTGGGAGGCAAGCCCGACCTGAGGC 2656
Qy 1089 aAla-----HisHis-----GluMe 1094
Db 2657 TGGGAGGCCCGGAGGGCGTCGACCTTCGCGCAGGACACACCGCGCACCGCAAGGA 2716
Qy 1094 tLysCysPro----- 1097

Db 2717 CAAGACCCCGCGCGCGGACCCAGGACCCAGGACCGAGCAGAGCGCCCGAAGCGGAGCGGGGA 2776
Qy 1098 -ProSerAlaArgSerSer-----ProHisSerProTrpSerAlaAlaSerSerTr 1114
Db 2777 GCCCGGTGCCCGGAGAGCGCGCGGCCGCGCACCGCAGCCACAGCAGGAGCGCGG-- 2834
Qy 1114 pThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArse 1134
Db 2835 ----GGGCGCCCGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2875
Qy 1134 rProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlnSerGlnAspGluG1 1154
Db 2876 CCCCGAGGCGCGCGCGCGCGCACCCAGCGCGCGCTCCCGGAGGAGCGCGCGCGCGGGA 2935
Qy 1154 u-----GluSerSerGluGluAspArgAlaSerPr 1164
Db 2936 GCGCGAGCGCACCGCGCGCGCACCGGCACAGGATCCGAGCAGAGGTGCCCGCGCGCAA 2995
Qy 1164 oAlaGlySerAspHisArgHisArgGlySerLeuGlu-----ArgGluAlaLysSe 1181
Db 2996 GCGCGAGCGCGCGCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 3055
Qy 1181 rSerPheAspLeuProAspThrLeuGlnValProGly-----LeuHisArgThrAlaSerG1 1200
Db 3056 CGGG-----GAGGAGCA 3094
Qy 1200 yArgSerSerAlaSerCln-----HisGlnAspCysAsnGlyLysSerAlaSerGlyAr 1218
Db 3095 GCGCGAGCTGCTCAGAGGCTGTGGAGAAGGAGACCCAGGAGAGGAGCGCGCGCGCGAG 3154
Qy 1218 gLeuAla-----ArgThrLeuArgThrAspProGlnLe 1230
Db 3155 GAGGCTGAGATAGTGAAGCCGACAGGAAGAGGAGCTCCGGAACCCAGCGCGCGGGA 3214
Qy 1230 uAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTr 1250
Db 3215 GCCACACTGTGACTGTGGAGACCTGTGGACTGTGACTGTGGGTCCC----- 3260
Qy 1250 pValArgSerArgLeuProAlaCysCysArgGluArg----- 1262
Db 3261 ----ATGCACACACTGCCAGCACCTGTCTCCAGAGGTGGAGGACAGCGCAGGAGTGC 3316
Qy 1263 -AspSerTrp----- 1265
Db 3317 AGCAATCAGCGGNA CGTCACTCGCATGGCGAGTCAAGCCCGCAGACCCGAACTATTGT 3376
Qy 1265 ----- 1265
Db 3377 ACATATCCAGTGATGTGACGGGCCCTCTTTGGGGAAGCAGCGTCTGCCAGTGGTAA 3436
Qy 1265 ----- 1265
Db 3437 CGTGGACCTGGAAGCCAGCAGAGGGGAAGAGGAGTGGAGCGGATGATGATGAG 3496
Qy 1266 -----SerAlaTyrIlePheProProGlnSerAr 1275
Db 3497 GAGCGCGCGCGCTATCGTCCATACAGCTCCATCTCTGTGTAAAGCCCGCAACCT 3556
Qy 1275 gPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuVa 1295
Db 3557 GCTCGCGCGCTTCTGCCACTACATCGTACCATGAGGTACTTCGAGGTGGTCACTTCGT 3616
Qy 1295 lIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe 1315
Db 3617 GGTATCCCTTGAAGAGCATCGCTGCTGTGTGAGGAGCCCA---GTGCGCACAGACTC 3673
Qy 1315 rAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaG1 1335
Db 3674 GCCCAGGAACACGCTCTGAATACCTGGATTACATTTTCACTGGTCTTTACTTTGA 3733
Qy 1335 uMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSe 1355
Db 3734 GATGGTATAAAGATGATCGACTTGGGACTGCTCTTCACTTCCCTGGAGCCTATTTCGCGGA 3793

Qy	1355	rSerTrpAsnValIleuaspGlyLeuValLeuIleSerValIleAspIleuValse	1375
Db	3794	CTTGTGAACATTTCTGGAC-----TTCAITTGTCAGTCGCCTGGTGGC	3841
Qy	1375	rMetVal--SerAspSerGlyThrLysIleLeuGlyMetLeuValLeuArgLeule	1394
Db	3842	GTTTGTCTTCTCAGGATCCAAAGGGAAGACATCAATACCATTCAAGTCTCTGAGAGTCT	3901
Qy	1394	uArgThrLeuArgProLeuArgValIleSerArgAlaInGlnGlyLeuLysLeuValGl	1414
Db	3902	TCGTGTCTCGGGCCCTCAAGACCATCAAACGGCTGCCCAAGCTCAAGGCTGTGTTGA	3961
Qy	1414	uThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleValIleCysalaPhePh	1434
Db	3962	CTGTGTGGTGAACCTCCCTGAAGAATGCTTCAACATCTTGATTGCTACATGCTCTTCAT	4021
Qy	1434	eIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGl	1454
Db	4022	GTTTCATATTTCCGTCATTCGGGTGCAGCTCTTCAAGGGAAGTTTTTCTACTGCACAGA	4081
Qy	1454	yGlu-----AspThrArgAsn-----IleThrAsnLysSerAspCy	1466
Db	4082	TGAATCCAAGAGCTGGAGAGGGACTCCAGGGGTCACTATTGGATTATCAGAAGAGGA	4141
Qy	1466	sAlaGluAlaSerTyArg--TrpValArgHisLysTyArgAsnPheAspAsnLeuGlyGl	1485
Db	4142	AGTGAAGCTTCAGCCAGGAGTGGGAAGAATAACGACTTTCATACGACAATGTGCTCTG	4201
Qy	1485	nAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyArS	1505
Db	4202	GGCTCTGCTGACGCTGTTCAGGTGCCAGGGAGAGGCTGGCCCCATGGTCTGTAACA	4261
Qy	1505	pGlyLeuAspAlaValGlyValAspGlnProIleMetAsnHisasnProTrpMetLe	1525
Db	4262	CTCCGTGGATGCCACCTATGAGGAGAGGTCGCAAGCCCTGGGTACCGCATGAGGTGC	4321
Qy	1525	uLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGl	1545
Db	4322	CATCTTCTACGTGTCTACTTTGTGGTCTTTCCTCTTCTTCGTCAACATCTTTGTGGC	4381
Qy	1545	yValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgAr	1565
Db	4382	TTTGATCATCATCACCTTC-----CAGAGCAGCGGGACAGAGTGAT	4423
Qy	1565	gArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMe	1585
Db	4424	GTCTGAA-----TGCAGCTGGAGAGAACGAGAGGGCTTGCACTTGCCTCGC	4471
Qy	1585	tAlaGluAlaGlnCysLysProTyTySerAspTyTySerArg-----PheArgLeule	1603
Db	4472	CATCAGCGCCAAACCCCTGACACGGTACATGCCCCCAAAACCGGAGTCGTCCAGTATAA	4531
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Qy	1816	pGlnGlu-----SerThrCysTyrAsnThrValIleSerProIleTyPheValSerPh	1834
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Qy	1997	--AlaaspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnPro	2015
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Job time : 1242 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 28, 2005, 13:23:23 ; Search time 1706 Seconds
(without alignments)

8160.926 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

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Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11980	99.6	6942	18	US-10-377-139-7 Sequence 7, Appli
2	11829	98.3	7285	10	US-09-383-894-3 Sequence 3, Appli
3	11673	97.0	7129	10	US-09-383-894-1 Sequence 1, Appli
4	10845.5	90.2	7648	18	US-10-377-139-10 Sequence 10, Appli
5	10845.5	90.2	7648	18	US-10-757-262-15 Sequence 15, Appli
6	10707	89.0	8116	17	US-10-062-674-2011 Sequence 2011, Ap
7	6103	50.7	3993	19	US-10-930-301-51 Sequence 51, Appli
8	5432.5	45.2	6990	18	US-10-377-139-8 Sequence 8, Appli
9	5420	45.1	6816	9	US-09-935-541-1 Sequence 1, Appli
10	5420	45.1	6816	16	US-10-425-800-1 Sequence 3, Appli
11	5420	45.1	6855	9	US-09-935-541-3 Sequence 3, Appli
12	5420	45.1	6855	16	US-10-425-800-3 Sequence 3, Appli
13	5407	45.0	6503	9	US-09-935-541-12 Sequence 12, Appli
14	5407	45.0	6503	16	US-10-425-800-12 Sequence 12, Appli
15	3950	32.8	5562	9	US-09-030-482B-18 Sequence 18, Appli
16	3861.5	32.1	6073	18	US-10-377-139-11 Sequence 11, Appli
17	1745.5	14.5	7362	17	US-10-375-253-11 Sequence 11, Appli
18	1743.5	14.5	7376	13	US-10-033-026-3 Sequence 3, Appli
19	1739.5	14.5	7364	9	US-09-954-456-1179 Sequence 1179, Ap
20	1739.5	14.5	7364	13	US-10-033-026-5 Sequence 5, Appli
21	1739.5	14.5	7364	18	US-10-736-883-31 Sequence 31, Appli
22	1739.5	14.5	7364	19	US-10-843-641A-4206 Sequence 4206, Ap
23	1732.5	14.4	6984	18	US-10-736-883-37 Sequence 37, Appli
24	1727	14.4	7175	17	US-10-375-253-13 Sequence 13, Appli
25	1726.5	14.4	7121	18	US-10-736-883-43 Sequence 43, Appli
26	1725	14.3	7185	18	US-10-736-883-39 Sequence 39, Appli
27	1721	14.3	7177	13	US-10-033-026-7 Sequence 7, Appli
28	1721	14.3	7177	18	US-10-736-883-33 Sequence 33, Appli
29	1720.5	14.3	6792	17	US-10-627-370-1 Sequence 1, Appli
30	1720	14.3	9695	18	US-10-736-883-27 Sequence 27, Appli
31	1720	14.3	9695	19	US-10-486-706-207 Sequence 207, App
32	1717.5	14.3	6083	13	US-10-029-413A-21 Sequence 21, Appli
33	1716.5	14.3	7713	18	US-10-736-883-41 Sequence 41, Appli
34	1693	14.1	7011	13	US-10-033-026-9 Sequence 9, Appli
35	1693	14.1	7011	18	US-10-736-883-29 Sequence 29, Appli
36	1686	14.0	7348	18	US-10-322-696-175 Sequence 175, App
37	1685.5	14.0	7291	18	US-10-322-696-83 Sequence 83, Appli
38	1685.5	14.0	7477	18	US-10-322-696-177 Sequence 177, App
39	1684.5	14.0	6572	18	US-10-467-491-1 Sequence 1, Appli
40	1682.5	14.0	7363	18	US-10-723-860-5192 Sequence 5192, Ap
41	1675.5	13.9	6503	18	US-10-377-139-16 Sequence 16, Appli
42	1674.5	13.9	7089	17	US-10-375-253-39 Sequence 39, Appli
43	1671	13.9	7032	17	US-10-375-253-37 Sequence 37, Appli
44	1667	13.9	9704	18	US-10-322-696-80 Sequence 80, Appli
45	1665.5	13.8	8490	15	US-10-101-510-617 Sequence 617, App

ALIGNMENTS

RESULT 1

US-10-377-139-7
; Sequence 7, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-10-377-139-7

Alignment Scores:

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 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 3
 Query Match: 99.60% Indels: 2
 DB: 18 Gaps: 0

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 DB 1756 GGGGTGGGAGTCTGTACACAGCTTCTACATGCTGACTGCCACTTGGAGCCAGTCCGTT 1815
 QY 600 ysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL 620
 DB 1816 GCCAGGACCCCTCCAGATGCCATCGAGGAGCATCTGGTAGGATGTGGGTAGTGGGA 1875
 QY 620 ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV 640
 DB 1876 AGGTGTACCCCTGTGCATACAGCCCTCCACAGAGATCTGAAGGATAAAGCACTAG 1935
 QY 640 alGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyP 660
 DB 1936 TGGAGGTGCCCCCAGCCCTGGGCCCCCCTCACAGCTTCAACATCCACCTCCGCTGGC 1995
 QY 660 roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC 680

Db 1396 CTTTCAGCTCCATGCACAGAGCTCTCTGGAGACACAGAGTACGGAGCCCTGCCATAGCTCCT 2055
Qy ySLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysp 700
Db GCAAATCTCAGGCCCTTCTCCAAAGGAGACAGTGGAGCCCTGGGGCCGACAGTTGTC 2115
Qy rofYrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAsps 720
Db CCTACTGTGCCGACAGGAGCAGAGAGCCAGAGTCCGCTGACCATGTCTATGCTGACT 2175
Qy erAspSerGluAlaValTrpGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspp 740
Db CAGACAGGAGCTGTGTATGAGTTTACACAGGACGCTCAGCAGCATGACCTCCGGGATC 2235
Qy roHisSerArgArgArgSerLeuGlyProAspAlaGluProSerSerValLeuA 760
Db CCCACAGCGCGGAGCAGCGAGCCCTGGGCCAGATGAGAGCCCTAGTTCTGTGTGG 2295
Qy laPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA 780
Db CTTTCTGAGGCTGATCTGTGACACATTCGGAGATCCGATAGATAGCAATACTTTGGCC 2355
Qy rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTrpHisGluG 800
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Qy lnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA 820
Db AGCCCGAGGAGCTCACCAGCGCCCTGGAAATCAGCAACATCGTCTTACCAGCGCTCTTCG 2475
Qy laLeuGluMetLeuLeuLysLeuValTrpGlyProPheGlyTrpIleLysAsnProT 840
Db CCTTGGAGATGCTGCTGAACTGCTTGTCTACGGTCCCTTTGGCTACATTAAGATCCCT 2535
Qy yrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnG 860
Db ACAACATCTTTGATGTGTCTATTGTGTCTATCAGTGTGGAGATTGTGGCCAGCAGG 2595
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Db GAGTGGCCCTGTGGTGTCTGGGACCTTCCGCCCTGATGGGGTGTCTGAAGCTGTGGCT 2655
Qy heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlar 900
Db TCCGTCCGGCCCTCAGCGCCAGCTCGTGTGTCTCATGAGACCATCGACAACTGGCCA 2715
Qy hrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeup 920
Db CTTTCTGCATGCTCCTCATGCTGTTCATCTTTCATCTTTCAGCATCCTGGGCATGCTCT 2775
Qy heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA 940
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Qy euMetThrPheGlyAsnTrpValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP 1000
Db TCATGACTTTTGGCAACTATGTGCTCTTAACTCTGTGGTGGCCATCTTGTGGAGAGAT 3015
Qy heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProServ 1020
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Qy luLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH 1060
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Qy isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrS 1080
Db ACCCAAGAGCTCCAGCACAGGTGTGGGGAAGCACTGGGCTCTGGCTCTCGACGTACCA 3255
Qy erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerA 1100
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1720 eulysLeuLeuLysMetAlaValIleGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL 1740
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5596 AGCCAAAGAGGAGGCGGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCC 5655
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6076 CTGGGGGCCCATCCCTAAACTACCCCACTGGCGCTCCCTCTGCTGTGCTCAGAGGCCCTC 6135
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2100 isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG 2120
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Db 6856 ACCCAACAGACATGGACCCC 6875

RESULT 2

US-09-383-894-3
; Sequence 3, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383.894
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098.004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117.399
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-3

Alignment Scores:

Pred. No.:	0	Length:	7285
Score:	11829.00	Matches:	2270
Percent Similarity:	97.72%	Conservative:	1
Best Local Similarity:	97.68%	Mismatches:	15
Query Match:	98.35%	Indels:	38
DB:	10	Gaps:	2

US-09-611-257A-24 (1-2287) x US-09-383-894-3 (1-7285)

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Qy 20 rgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
Db 117 GCCCCTCTTCGAGCCCCCGGGGCCCCGGCTGGCCAGAGGATGGACGAGGAGGATGG 176

Qy 40 luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProG 60
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Db 237 GGGCGGGGGCGGCGAGGGCGGGGTCCGACGAAAAAGGACCCGGGCGACGCGGACTCCGA 296
Qy 79 uAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAs 99
Db 297 GGGGAGGGGCTCCGCTACCCGGCGCTAGCCCGGTGGTTTCTTCTACTTGAAGCCAGGA 356
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Db 477 TGCTGTGACTCCAGCGCTGCCGGATCCTGCAGGCCCTTCGATGACTTCATCTTTGCCCT 536
Qy 159 ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysT 179
Db 537 CTTTGTCTGTGAATGGTGTGAAGATGGTGGCTTGGGCATCTTTGGGAAGAAATGTTA 596
Qy 179 rLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluT 199
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Db 777 CTTGCGCTATGCTGGCAACGTCCTGCTGCTCTGCTTCTTCTTTTTCATCTTTGCGAT 836
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 ; Publication No. US20030125269A1
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 ; APPLICANT: Li, Ming
 ; TITLE OF INVENTION: T-Type Calcium Channel
 ; FILE REFERENCE: 004, 00191
 ; CURRENT APPLICATION NUMBER: US/09/383,894
 ; CURRENT FILING DATE: 1999-08-26
 ; EARLIER APPLICATION NUMBER: US 60/098,004
 ; EARLIER FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: US 60/117,399
 ; EARLIER FILING DATE: 1999-01-27
 ; NUMBER OF SEQ ID NOS: 11
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Fri Apr 29 11:30:22 2005

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 3902 AAATGACCCACAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACTCATCTTACGG 3961
 1330 laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluG 1350
 3962 CAGTCTTTCTAGCTGAAATGACAGTGAAGTGGTGGCACCTGGGCTGGTCTTGGGAGC 4021
 1350 lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI 1370
 4022 AGGCTTACCTGCGCAGCAGCTGGAATGTCTGGACGGCTTGTGCTGCTCATCTCCGTC 4081
 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
 4082 TCGACATCTGCTCTCCATGGTCTCCGACAGCGGCACCAAGATCTTGGCATCTTGAGGG 4141
 1390 alLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgIleGlnGlyLeuL 1410
 4142 TGCTGGCGCTGCTGGGACCCCTGCTCCACTCAGGGTCTATCAGCGGGCCCGGAGCTGA 4201
 1410 yslLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC 1430
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 1430 yscysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
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 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaA 1470
 4322 TCGTGTGTCAGGTCAGGACACAGCAACATCATAACAAATCCGACTCGCTGAGGCCA 4381
 1470 erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
 4382 GCTACCGATGGTGGTCCGCAACAGTCAACTTTGACAACTGGGCCAGGCTCTGATGTCC 4441
 1490 euPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlav 1510
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 1510 alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS 1530
 4502 TGGGTGTGGATCAGAGCCCATCATGAACCAACCCCTGGATGCTGCTATCTTCACTCT 4561
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 4562 CCTTCTCTCATCGTGGCTCTTCTTGTCTGAAACATGTTTGTGGGCTGGTGGTGAGA 4621
 1550 snPheHisLysCysArgGlnHisGlnGlnGluGluAlaArgArgArgGluGluLysA 1570

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Qy 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
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Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
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Qy 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
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Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
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Qy 1979 rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT 1999
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Qy 2219 erIleSerIleAspProGluSerGlnGlySerArgProProCysSerProGlyValC 2239
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Qy 2239 ysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuA 2259
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 QY 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS 1919
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 US-10-757-262-15
 ; Sequence 15, Application US/10757262
 ; Publication No. US20040197825A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Karicheti, Venkateswarlu
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; APPLICANT: Eliasof, Scott D.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
 ; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
 ; TITLE OF INVENTION: 33751, 52872, 14063, 22079, 32544, 43239, 44373, 51164,
 ; TITLE OF INVENTION: 53010, 16852, 1587, 22079, 22245, 2387, 52908, 69112, 14990,
 ; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
 ; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
 ; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
 ; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
 ; TITLE OF INVENTION: 55053
 ; FILE REFERENCE: MP103-007P1RNOMNIM
 ; CURRENT APPLICATION NUMBER: US/10757,262
 ; CURRENT FILING DATE: 2004-01-14
 ; PRIOR APPLICATION NUMBER: US 60/440,318
 ; PRIOR FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: US 60/444,783
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: US 60/457,901
 ; PRIOR FILING DATE: 2003-03-27
 ; PRIOR APPLICATION NUMBER: US 60/468,775
 ; PRIOR FILING DATE: 2003-05-08
 ; PRIOR APPLICATION NUMBER: US 60/471,614
 ; PRIOR FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: US 60/478,742
 ; PRIOR FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: US 60/488,529
 ; PRIOR FILING DATE: 2003-07-18
 ; PRIOR APPLICATION NUMBER: US 60/491,156
 ; PRIOR FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US 60/499,594
 ; PRIOR FILING DATE: 2003-09-02
 ; PRIOR APPLICATION NUMBER: US 60/506,332
 ; PRIOR FILING DATE: 2003-09-26
 ; NUMBER OF SEQ ID NOS: 136
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 ; SEQ ID NO 15
 ; LENGTH: 7648
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(7134)
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 Percent Similarity: 89.72% Conservative: 33
 Best Local Similarity: 88.33% Mismatches: 110
 Query Match: 90.17% Indels: 135
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 Db 2 TGGACGAGGAGGAGATGGAGCGGCGCCGAGAGTCCGACACAGCCCCCGAGCTTCATGC 61
 Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGlyLysAsp 73

Db 62 GGCTCAACGACCTGTGCGGGGCGCGGGGCGCGGGGCGCGGGTTCAGCAGAAAAGGACC 121
QY 73 roGlySerAlaAepSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGGAGCTCCGAGGGGAGGGGCTGCCGTACCCGGCGTGGCCCCGGTGGTTT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAAGCAGGACAGCGCGCGCGAGCTGGTGTCTCCGCGACGGTCTGTAAAC 241
QY 113 roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTTGAAGCCATCAGCATGTTGGTCATCTTCTCAACTGCGTGACCCCTGGGCACTG 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATGCGAGGACATCGCTGTGACTCCCGAGCGCTCCCGATCTCTGCGAGCGCTTG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValIleValIleValIleValI 173
Db 362 ATGACTTCACTTGTGCTTCTTTGCGGTGAGATGGTGTGAAGATGGTGGGCTTGGGCA 421
QY 173 lePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAGTGTACTTGGGAGACACTTGGAAACCGGCTTGACTTTTTCATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGATGCTGGAGTACTGCTGACCTGACGACGAAACGTCAGCTTCTCAGCTGTGAG 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGGTGGCCAGATCGCATCCCTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCAGTTGCTGTGGATACGCTGCCATGCTGGGCAACGTCCTGCTGCTGCTCTCTCTG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnIleuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCACTTTCGGCATCGTCCGCGTCCAGCTGTGGGCGAGGCGTCTTCGGAACCGAT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnf 293
Db 722 GCTTCTTACCTGGAATTTTCAAGCTCCCTTGAGCGTGGACCTGGAGCGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMecArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGAGAAGCGTCCCAAGCTGCGGGGACGGGGCGGTGGCCCACTTGGCGGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGCCCTACAAGCTCCAGCAACACCACCTGTGTCACTGGAAACGAGTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCAACTTTTGACAAACATTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCTGATCGCCATCTTCCAGGTCATCAGCTGGAGGGCTGGGTGCACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleV 413
Db 1082 ACTTTGTGATGATGCTCATTTCTTACATTTTCACTTCACTTCACTCTCTCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTATGATCAACCTGTGCTGGTGGTGAATGGCCACGAGTTCTCAGAGA 1201

QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGAAGCCAGCTGATGCGGGAGCAGCTGTGCGGTCTCTGTCCACAGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGGCTAGCTTCTCTGAGCCCGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTTCTGTAAGCAGCCCGCAGCTGGCTCAGGTCCTCTCGGGCAGCAGGTGTC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCGACCCCTCGGGGGCAGAGACCCAGCCAGCCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTCGCTCCCGCCCGCTATCCGTCCACCATCTGGTGCACCAACCAACCA 1501
QY 533 isHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCACTTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGACAGGATGCCAATGGTCCCGCAGGCTCATGCTGCCACCACTCCGAGCCCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCCTCTCCGGGCCCCCTCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCG 1681
QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GGCATTTAGACGAGTCCGCTGCCAGGGCCCCCTCCAGGTCCTCCCATCTGAGGCGAT 1741
QY 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGGACTGTGGCAGCGGAGAGGTATCCACCGTGCACACCAAGCCCTCCACGGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluAlaProProProProProProProProProPro 653
Db 1802 CGCTGAAGGAGGAGGACCTAGTAGAGTGGCTGCCAGCTCTGGGGCCCCCAACCCCTACA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCTCAACATCCACCCGGGCCCCCTACAGCTCCATGCACAAAGCTGTGGAGACACAGAT 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTGCCAAAGCTCTTCAAGATCTCCAGGCTTGTGTAAGCAGACAGTGGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGCTCAGACAGCTGCCCTACTGTGCCGGGCGGGGAGGGAGGTGGAGCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCAGCCGTGAATGCTTGAATCTCAGCAGCGAGGAGCTTATGAGTTTACACAGGATGCC 2101
QY 733 lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCAGCTCCGGGACCCCGACAGC---CGGGCGAACGGAGCCCTGGGGCCAGATG 2158
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCAGCTCTGTGCTGGCCCTCTGAGAGGCTAATCTGTGACACTTCCGAAAGATTG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAGTACTTTGGCCGGGGAATCATGATGCCATCTCTGCTCAACACACTCAGCA 2278

Qy	793	etGlylleGluTyRhiSgluInProGluInLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2279	TGGGCATCGAATACACAGCAGCGCCGAGAGCTTACCAACGCGCTAGAAATCAGCAACA	2338
Qy	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyRGlyProp	833
Db	2339	TCGTCTTCACAGAGCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTTGTGTATGGTCCCT	2398
Qy	833	heGlyTyRlleLysAsnProTyRAsnIlePheAspGlyValIleValValIleSerValR	853
Db	2399	TTGCTACATCAAGAATCCCTACAAACATCTTCGATGCTGTCAATTTGTGTGTCATCAGCGTGT	2458
Qy	853	rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCGTGGGCGACAGCGGGCGCGCTGTGCTGCTGCGAGACCTTCGCGCTCATGC	2518
Qy	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2519	GTGTGCTGAAGCTGGTGGCTTCTGCGCGCGCTGACGCGCGAGCTGGTGGTGTCTATGA	2578
Qy	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2579	AGACCATGGACAGCTGCCACCTTCTGCGATGCTGCTTATGCTCTTTCATCTTCATCTTCA	2638
Qy	913	erlleLeuGlyMetHisLeuPheGlyCysIysPheAlaSerGluArgAspGlyAspThrL	933
Db	2639	GCATCTGGGCATGCATCTCTTCGGCTGCAAGTTTGCTCTCGACGGGATGGGACACCC	2698
Qy	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCCGGAAGAAATTTTGACTCTTGTCTGGGCCATCTGTCATCTCTTTTCAGATCC	2758
Qy	953	euThrGlnGluAspTrpAsnLysValLeuTyRAsnGlyMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCCAGGAGGACTGGAAACAAAGTCTCTTACAAATGGTATGGCTCCACGTGCTCTGGG	2818
Qy	973	laAlaLeuTyRPhelAlaLeuMetThrPheGlyAsnTyRValLeuPheAsnLeuLeuV	993
Db	2819	CGGCGCTTTATTTTCATTTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAAATTTGCTGG	2878
Qy	993	alAlaIleLeuValGluGlyPheGlnAlaGlu-----	1003
Db	2879	TCGCCATCTTGTGGAGGGCTTCAGCGCGAGGAATCAGCAACGGGAAGATGCGAGTG	2938
Qy	1004	-----GlyAspAlaThrLysSerG	1010
Db	2939	GACAGTTAAGCTGTATTACGCTGCTGCACTCCAGGGGGGAGATGCCACAGTCCG	2998
Qy	1010	luSerGluProAspPheSerProSerValAspGlyAspGlyAspArgLysArgL	1030
Db	2999	AATCAGAGCCCGATTTCTTCTTCAACCCAGCTGGATGCTGATGGGACAGGAAGAAGTCT	3058
Qy	1030	euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuI	1050
Db	3059	TGGCCTTGTGTCTCCCTGGGAGACACCGGAGCTGCGGAAAGAGCTGCTGCCGCTCTCA	3118
Qy	1050	lelleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG	1070
Db	3119	TCATCCACAGCGCGCCACACCCATGCTGCCCAAGAGCACCGACCGGGCTCTGGGCG	3178
Qy	1070	luAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA	1090
Db	3179	AGGCGCTGGGCGCTCGCTCGCGCGCACACAGCAGCGGGTTCGGCAGAGCCTTGGGCGG	3238
Qy	1090	laHisHisGluMetLysCyBProProSerAlaArgSerSerProHisSerProTrpSerA	1110
Db	3239	CC-----CACGAGATGAAGTCAACGCGCCAGCGCCCGCAGCTCTCCGCACAGGCCCTTGGAGCG	3295
Qy	1110	laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL	1130
Db	3296	CTGCAAGCAGCTGGACACAGCAGGCGCTCCACCGGGAACAGCTCTCGGCGGTGCACCCAGCC	3355
Qy	1130	euLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluS	1150

3356	Db		TGAAGCGGAGAACCCAAAGTGGAGCGCGGTCCCTTGTGTGGGAGAGGCCAGAGA	3415
1150	Qy	erGlnAepGluGluGluSerSerGluGluAepArgAlaSerProAlaGlySerAspHisA	1170	
3416	Db	GCACAGNTGAAGAGGAGAGCTCAGAGAGAGCGGGCCAGCCCTGCGGGCAGTGACCATC	3475	
1170	Qy	rgHisArgGlySerLeuGluAArgGluAlaLysSerSerPheAepLeuProAaspThrLeuG	1190	
3476	Db	GCCACAGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCACACACTGCG	3535	
1190	Qy	lnValProGlyLeuHisAArgThrAlaSerClyArgSerSerAlaSerGluHisGlnAepC	1210	
3536	Db	AGTGCCAGGGCTGCATCGCACATGCCAGTGGCCGAGGGTCTGCTTCTGAGCACGAGACT	3595	
1210	Qy	ysAenGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuAArgThrAspAaspProGlnL	1230	
3596	Db	GCAATGGCAAGTGGCTTCAGGGGGCTGGCCCGGGCCCTGCGGCCGTATGACCCCCAC	3655	
1230	Qy	euAepGlyAaspAaspAsnAaspGluGlyAenLeuSerLysGlyGluAArgIleAlaAt	1250	
3656	Db	TGGATGGGATCAGCCGATGACGAGGCCAACCTGAGCAAAAGGGAAACGGGTCCGCGCT	3715	
1250	Qy	rpValArgSerArgLeuProAlaCysCysArgGluAArgAaspSerTrpSerAlaTyrIleP	1270	
3716	Db	GGATCCAGGCCGACCTCCCTGCTGCTCGACGAGAGACTCCTGGCTAGCCTACATCT	3775	
1270	Qy	heProProGlnSerArgPheArgLeuLeuCyHisAArgIleIleThrHisLysMetPheA	1290	
3776	Db	TCCCTCTCAGTCCAGGTTCCGCTCTGTGTACCGGATCNCACCCACAGATGTTGCG	3835	
1290	Qy	sphisValValLeuValIleIlePheLeuAenCysIleThrIleAlaMetGluArgProL	1310	
3836	Db	ACCAGTGGTCTTGTCATCATCTTCTTAACTGCATCACCATCGCCATGGAGGCCCCA	3895	
1310	Qy	ysIleAepProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA	1330	
3896	Db	AAATGTACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTCA	3955	
1330	Qy	laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCyPspheGlyGluG	1350	
3956	Db	CAGTCTTTCTGGCTGAANAATGACAGTGAGGTGGTGACACTGGGCTGGTCTTGGGAGC	4015	
1350	Qy	lnAlaTyrLeuArgSerSerTrpAsnValLeuAaspGlyLeuLeuValLeuIleSerValI	1370	
4016	Db	AGCGTACCTCGGAGCAGTTGGAACGTGTGGACGGGCTGTTGGTCTCATCTCCGTCA	4075	
1370	Qy	leAepIleLeuValSerMetValSerAaspSerGlyThrLysIleLeuGlyMetLeuArgV	1390	
4076	Db	TCGCACATCTCGTGTCTCATGTGCTCTGCACAGCGCACCAAGATCCTGGGCATGCTGAGG	4135	
1390	Qy	alLeuArgLeuLeuAArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL	1410	
4136	Db	TGCTGGCGGTGCTGCGGACCCCTGGCCCGCTCAGGGTGATCAGCCGGCGCGAGGGCTGA	4195	
1410	Qy	ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC	1430	
4196	Db	AGCTGGTGGTGGAGACGCTGATGTCTCACTGAAACCCATCGGCAACATTGTAGTCACT	4255	
1430	Qy	ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP	1450	
4256	Db	GCTGTGCTCTTCTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAAGGGAAGTTT	4315	
1450	Qy	heValCysGlnGlyGluAaspThrArgAsnIleThrAenLysSerAaspCysAlaGluAla	1470	
4316	Db	TCGTGTGCCAGGGCGAGATACACGAAACATCACCAATAATCGACTGTGCCGAGGCCA	4375	
1470	Qy	erTyrArgTrpValArgHisLysTyrAsnPheAaspAsnLeuGlyGlnAlaLeuMetSerL	1490	
4376	Db	GTTACCGGTGGTCCGSCACAGGTACAACTTTGACAACTTTGGCACCTTTGGCACGSCCT	4435	
1490	Qy	euPheValLeuAlaSerLysAaspGlyTrpValAepIleMetTyrAaspGlyLeuAaspAlav	1510	

4436	TGTTCTGTTTGGCCCTCCAAAGGATGGTTGGGTGGACATCATGTACAGTGGCGCTGGATGCTG	4495
1510	alGlyValAaspGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleS	1530
4496	TGGCGTGGACAGCAGCCCATCATGAACACACAAACCCCTGGATGCTGCTGTAATCTCATCT	4555
1530	erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluA	1550
4556	CGTTCTCTGCTCATTTGTGGCCCTCTTTGTCTGAACATGTTTGTGGGTGGTGGTGGA	4615
1550	snPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysA	1570
4616	ACTTCCACAAGTGTGGCAGCACGAGGAAAGAGAGGCCCGCGCGGAGGAGAAAC	4675
1570	rgLeuArgArgLeuGluLysLysArgArg-----	1579
4676	GCCTACGAAGACTGGAGAAAAGAGAAGAATCTAATGCTGGACGATGTAATTTGCTTCG	4735
1580	--SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA	1599
4736	GCAGCTCAGCCAGCGCTGAGAGCCAGTGCAAAACCTTACTACTCGACTACTCCC	4795
1599	rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG	1619
4796	GCITTCGGCTCTCGTCCACCACTTGTGACCAAGCCACTACCTGGACCTCTTCATCACAG	4855
1619	lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL	1639
4856	GTGTCACTGGCGCTGAACGTGTCACCATGGCCATGGAGCACTACCAAGCCGCCAGATC	4915
1639	euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV	1659
4916	TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTTGTCTGGAGTCAG	4975
1659	alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrPAsnGlnLeuA	1679
4976	TTTTCAAACTTGTGGCCCTTGGTTTCGTCGCTGGTTCTTCCAGGACAGGTGGAACACAGCTGG	5035
1679	spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL	1699
5036	ACCTGGCCATTTGCTGCTGCTTCATCAITGGGCATCAGCTGGAGGAATCGAGGTCAACG	5095
1699	euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV	1719
5096	CCTCGCTGCCCATCAACCCCAACCATCATCGCATCATGAGGGTGTCTGCGCATTTGCCCGAG	5155
1719	alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA	1739
5156	TGCTGAAGCTGCTGAAGATGCTGTGGCATGCGGGCGCTGCTGGACACCGTGTATCGAGG	5215
1739	laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759
5216	CCCTGCCCCAGTGGGAAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGCGAG	5275
1759	laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL	1779
5276	CTCTGGCGGTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCC	5335
1779	euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVals	1799
5336	TGGGCCGTGTCAGCCACCTTTTCGGAACCTTTGGCATGGCCCTTCTTAACCCCTCTTCGAGTCT	5395
1799	erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS	1819
5396	CCACAGGTGACAAATGGAAATGGCAATATGAAGGACACCCCTCCGGGACTGTGACACAGAGT	5455
1819	erThrCysTyrAsnThrValIleSerProIleTyrPheValIserPheValLeuThrAlaG	1839
5456	CCACCTGCTACAAACAGGTCAATCTGCCCTAICTACTTGTGTCTCTGCTGCTGACGGCCC	5515
1839	lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL	1859
5516	AGTTCTGCTGTAATCAACGTGGTGTATGCGCTGCTGATGAACACCTCGAGAGAGAACAA	5575

1859	Qy	ysGluAlaIysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetIysThrLeus	1877
5576	Db	AGGAGGCCAAGGAGGAGGCGGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTCA	5635
1879	Qy	erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA	1899
5636	Db	GCCTCCAGAGCCCACTCGCCACTGGGAGAGCCCTTCTCTGGCCTGGGTCGAGGGCCCG	5695
1899	Qy	snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAAs	1919
5696	Db	ACAGCCCGACGACGCCCAAGCCTGGGCTCTGCACCCAGCGGCCACGCGAGATCAGCCT	5755
1919	Qy	erGlyPheSerLeuGluHisProThr	1927
5756	Db	CCCACTTTTCCCTGGAGCACCCACACGACAGGCAGCTGTTGACACCATATCCCTGCTCA	5815
1927	Qy	-----	1927
5816	Db	TCCAGGGCTCCCTGGAGTGGGAGCTGAAGCTGATGGACGAGCTGGCAGGCCACAGGGGGCC	5875
1927	Qy	-----	1927
5876	Db	AGCCTCTGCCCTTCCCTTCTGCCCCAGCGCTGGAGGCTCCGACCCACAGATCCCTCTCTAG	5935
1927	Qy	-----	1927
5936	Db	CTGAGATGGAGGCTCTCTCTGACGTACAGAGATTGTGTGAACCGTCTGCTCTCTCTAG	5995
1927	Qy	-----	1927
5996	Db	CTCTGACCGATGACTCTTTGCCCTGATGACATGCACACACTTTACTTAGTGCCCTCGAGA	6055
1928	Qy	-----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV	1946
6056	Db	GCAATATGCAGCCCCACCCACGAGCTGCCA-----GGACGACATTACTGACTG	6106
1946	Qy	alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA	1966
6107	Db	TGCGGAAGCTGGGGTTCAGCCGAAGCACCTCTCTGCCAATGACAGCTACATGTGTGCGC	6166
1966	Qy	snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnS	1986
6167	Db	ATGGGAGCACTCGCGAGGGGCCCCCTGGGACACAGGGGCTGGGGGCTCCCCAAGCTCAGT	6226
1986	Qy	erGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeup	2006
6227	Db	CAGGCTCCGCTTGTTCGGTTCACTCCACAGCCAGCAGATACACAGCTACATCTGCAGCTTC	6286
2006	Qy	roLysAspValHisThrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL	2026
6287	Db	CCAAAGATGCACCTCATCTGTCTCCAGCCCCACAGCGCCCCAACCTGGGGGACCATTCCCCA	6346
2026	Qy	ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI	2046
6347	Db	AACTGCCCCCAACAGGAGCGTCTCCCTTTGGCTCAGAGGCCACTCAGCGCCACGACGCAA	6406
2046	Qy	leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV	2066
6407	Db	TAAGGACTGACTCCTTTGAGCGTTTCAGGGTCTGGGAGCTGGGAGAGACCTGCTGGCAGGG	6466
2066	Qy	alSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleG	2086
6467	Db	TGAGTGGGCCCCCTCCCGCCCCCTGGCCGGGCGCTACTCTTTCTGGGGCCAGTCAAGTACCC	6526
2086	Qy	lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlap	2106
6527	Db	AGGCACACGACGACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCC	6586
2106	Qy	roCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuG	2126
6587	Db	CTTGCCAGGCCCAGAACCCCAACTGGGCGAAGGGCCCTCCAGAGACAGAGACGAGCTTAG	6646

Qy 2126 luLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGluG 2145
 Db |||||
 6647 AGTTGGACACGGAGCTGAGCTGGATTTCAGAGACCTCTCTGCCCCCTGGCGGCAGGAGG 6706
 Qy 2145 luProLeuPheProArgAspIleuLysCysTyrSerValGluThrGlnSerCysArgA 2165
 Db |||||
 6707 AGCCCCCATCCCCACGGGACCTGAAGAAGTGCTACAGCGTGGAGGCCAGAGCTGCCAGC 6766
 Qy 2165 rgArgProGlyPheTrpLeuAspGluGlnArgHISerIleAlaValSerCysLeuA 2185
 Db |||||
 6767 GCCGGCTAGCTCTGCTGGATGAGCAGAGAGACACTCTATCGCCGTGAGCTGCCCTGG 6826
 Qy 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205
 Db |||||
 6827 ACAGCGCTCCCAACCCACCTGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTG 6886
 Qy 2205 lyGlyProGlySerArgProIlyLysLysLeuSerProProSerIleSerIleAspProp 2225
 Db |||||
 6887 GGGGGCTGGGAGCGCGCCCAAGAAAAAAGCTCAGCCCGCCTAGTATCACCATAGACCCCC 6946
 Qy 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlap 2245
 Db |||||
 6947 CCGAGACCAAGGTCCTCGACCCCGCCAGCCCTGGTATCTGCTCCGAGGAGGGCTC 7006
 Qy 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265
 Db |||||
 7007 CGTCCAGGACTCAAGATCCCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCCTCG 7066
 Qy 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA 2285
 Db |||||
 7067 CCTCCCCAAGAAAGATGTGTGAGTCTCTCCGGTTTATCTCTGACCCAGCAGACCTGG 7126
 Qy 2285 spPro 2286
 Db |||||
 7127 ACCCC 7131

RESULT 6

US-10-062-674-2011
 ; Sequence 2011, Application US/10062674
 ; Publication No. US20040005559A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
 ; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
 ; FILE REFERENCE: PA-0026-1 CIP
 ; CURRENT APPLICATION NUMBER: US/10/062,674
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 2002-01-102
 ; PRIOR FILING DATE: 2000-07-24
 ; NUMBER OF SEQ ID NOS: 2217
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2011
 ; LENGTH: 8116
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20040005559A1 404183.1
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1) ... (8116)
 ; OTHER INFORMATION: a, t, c, g, or other
 US-10-062-674-2011

Alignment Scores:

Pred. No.: 0 Length: 8116
 Score: 10707.00 Matches: 2098
 Percent Similarity: 89.92% Conservative: 52
 Best Local Similarity: 87.75% Mismatches: 130
 Query Match: 89.02% Indels: 112
 DB: 17 Gaps: 6

US-09-611-257A-24 (1-2287) x US-10-062-674-2011 (1-8116)

Qy 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
 Db |||||
 321 CCGCCGGGGCCCCCGGTTGCGTGAGGACACCTCTCTGAGGGGCGCGCTTGGCCCTCT 380
 Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla 42
 Db |||||
 381 CCGGATCGCCCGGGGCCCCCGCTGGCCAGAGATGGACGAGGAGGAGATGGAGCGGGCG 440
 Qy 43 ProArgSerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGly 62
 Db |||||
 441 CCAGAGATCGGAGACGCCCGGAGCTTCATGGGGCTCAACGACCTCTCGGGGGCGGGG 500
 Qy 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
 Db |||||
 501 GCCCGCGGGCGCGGGTTCAGCAGAAAAAGACCCGGGCGAGCGGACTCCGAGGCGGAGG 560
 Qy 82 lyLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
 Db |||||
 561 GGCTGCGGTACCCCGGCGCTGGCCCGGTGGTCTTCTTCTACTTTGAGCCAGGACGCGCC 620
 Qy 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
 Db |||||
 621 CGCGAGCTGGTGTCTCCGACCGGTCTGTAAACCCCTGGTTTGGAGCGCATCAGATGTGG 680
 Qy 122 alileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
 Db |||||
 681 TCATCCTTCTCAACTCGGTGACCTTGGGCATGTTCCGGCCATCGCAGGACATCGCCTGTG 740
 Qy 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlav 162
 Db |||||
 741 ACTCCAGCGCTCCCGGATCCTCGAGGCTTTGATGACTTTCATCTTTTTCCTTTTTCGCG 800
 Qy 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
 Db |||||
 801 TGGAGATGGTGAAGATGTTGGGCTTGGGCATCTTTGGGAAAAAGTGTTACTCTGGAG 860
 Qy 182 spThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGlyTrpSerLeuA 202
 Db |||||
 861 ACATTGGAAACCGCTTGACTTTTTCATCGTCATCGCAGGATGCTGGAGTACTCGCTGG 920
 Qy 202 spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
 Db |||||
 921 ACCTGAGAAACGTGAGCTTCTCAGCTGTTCAGGACAGTCCGTGTGCTGCGACCGCTCAGG 980
 Qy 222 laileAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM 242
 Db |||||
 981 CCATTAAACCGGGTGGCCAGCATCGCATCTTGTACGTTGCTGCTGGATACGCTGCCCA 1040
 Qy 242 etLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV 262
 Db |||||
 1041 TGCTGGGCAACGTCCTGCTCTGCTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTGCG 1100
 Qy 262 alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP 282
 Db |||||
 1101 TCCAGCTGTGGGAGGCGCTTCTCGGAAACCGATGCTTCTTCTTCTTCTTCTTCTTCTTCTT 1160
 Qy 282 roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI 302
 Db |||||
 1161 CCCTGAGCGTGGACCTCGAGCGCTATTACACAGAGAGAACGAGGATGAGAGCCCCCTTCA 1220
 Qy 302 leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG 322
 Db |||||
 1221 TCTGCTCCAGCCACCGGAGAACGGCATGGGCTCTGTCAGAGAGGTCGCCACGCTGCGCG 1280
 Qy 322 lyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerA 342
 Db |||||
 1281 GGGACGGGGCGGTGGGCCACCTTGGGCTTGGACTATGAGGCTTACAGAGCTCCAGCA 1340
 Qy 342 snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisenp 362
 Db |||||
 1341 ACACCACTGTGTCAACTGGAAACAGTACTACCACTACTGCTCAGCGGGGAGCACAACC 1400
 Qy 362 roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV 382

[illegible]

Db	6947	CCAGGACAGCAGCACTCCCGCAGCCACGACCAAGATCTCCAAGACATGATCCCGCCAG	6900
Qy	2105	laProCysProGlyLeuGluProSerTrpAlaIysAspProProGluThrArgSerSerL	2125
Db	6907	CCCTTGCCAGGCCAGAACCCAACTGGGGCAAGGGCCCTCCAGAGACGACGAGCAGCT	6966
Qy	2125	euGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnG	2144
Db	6967	TAGAGTTGGACACGGAGCTGAGCTGGATTTACAGAGACCTCTGCGCCCTGGCGGCCAG	7026
Qy	2144	luGluProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCysA	2164
Db	7027	AGGAGCCCCATCCACACGGGACCTCAAGAAAGTGCTACAGCGTGGAGGCCACGAGCTGC	7086
Qy	2164	rgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysL	2184
Db	7087	AGCGCCGGCCCTGCTCTGCTGGATGACAGAGGAGACACTCTATCGCGCTCAGCTGCC	7146
Qy	2184	euAspSerGly-SerGlnProArgLeuCysProSerProSerSerLeuGlyGlnPro	2203
Db	7147	TGGACAGCGGCTTCCCAACCCACCTGGGCACAGACCCCTCTAACCTTGGGGCCAGCCT	7206
Qy	2204	LeuGlyGlyProGlySerArgProGlyLysLeuLysLeuSerProProSerIleSerIle-As	2223
Db	7207	CTTGGGGGGCCCTGGAGCCCGGCCCAAGAAAACTAGCCCGCTAGTATCACCATAGA	7266
Qy	2223	pProProGluSerGlnGlySerArgProProCysSerPro-GlyValCysLeuArgA	2243
Db	7267	CCCCCCCCGAGAGCCCAAGGTCTCTGGAGCCCGCCAGCCCTTGGGTNTCTGCTCCGGAGGA	7326
Qy	2243	rgAlaProAlaSerAspSerLysAspProSerValSer--SerProLeuAspSerThrAl	2262
Db	7327	GGGTCTCGTCCAGGCACTCCAAGATCCCTTGGCTCTGGGCCCCCTGAACAGCATGGC	7386
Qy	2262	aAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerSerProTh	2282
Db	7387	TGCTCGCCCTCCCCAAAGAAAGATGTCTGCTGAGTCTCTCCGGTTTATCTCTGACCCAGC	7446
Qy	2282	rAspMetAspPro 2286	
Db	7447	AGACTGGAGCCCC 7459	
RESULT 7			
US-10-930-301-51			
; Sequence 51, Application US/10930301			
; Publication No. US20050026207A1			
; GENERAL INFORMATION:			
; APPLICANT: Issa, Jean-Pierre			
; TITLE OF INVENTION: CACNAIG POLYNUCLEOTIDE POLYPEPTIDE AND			
; FILE OF INVENTION: METHODS OF USE THEREFOR			
; FILE REFERENCE: JHU1590			
; CURRENT APPLICATION NUMBER: US/10/930,301			
; CURRENT FILING DATE: 2004-08-30			
; PRIOR APPLICATION NUMBER: US/09/398,522			
; PRIOR FILING DATE: 1999-09-15			
; NUMBER OF SEQ ID NOS: 120			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 51			
; LENGTH: 3993			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: CACNAIG - a gene encoding a T-type calcium channel			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (373)...(3993)			
US-10-930-301-51			

Alignment Scores:			
Pred. No.:	0	Length:	3993
Score:	6103.00	Matches:	1173
Percent Similarity:	95.4%	Conservative:	12
Best Local Similarity:	94.5%	Mismatches:	52

Query Match:	50.74%	Indels:	4
DB:	19	Gaps:	2
US-09-611-257A-24 (1-2287) x US-10-930-301-51 (1-3993)			
Qy	3	ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer	22
Db	281	CGCGGGGGCCCCGGGTGGCGTAGGACACCTCTCTGAGGGGGCGCGCTTGGCCCTCT	340
Qy	23	SerAspProProGlyProArgLeuAlaArgGlyThrThrArgArgMetGluArgAla	42
Db	341	CCGATCGCCGGGGCCCCGGCTGGCCAGAGATGGACAGGAGGATGGAGCGGGCG	400
Qy	43	ProArgSerArgAspSerProValAlaSerArgSerThrThrCysProGlyProGly	62
Db	401	CCGAGGAGTCGGACACGCCCGGAGCTTCATCGCGCTCAACGACCTGTCGGGGCGGGG	460
Qy	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu	82
Db	461	GCCGGCGGGGGCGGGGTTCAGCAGAAAAGGACCCGGGCGAGCGGACTCCGAGCGGAGG	520
Qy	82	lyLeuProTyProAlaAlaAlaProValValPhePheThrLeuSerGlnAspSerArgp	102
Db	521	GGCTGCCGTACCCGGCGCTGGCCCCGGTGGTTTCTTACTTGAGCCAGACAGCGCC	580
Qy	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	122
Db	581	CGCGAGCTGGTGTCTCCGACGGTCTGTAAACCCCTGGTTGAGCGCATCAGCATGTGG	640
Qy	122	alleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142
Db	641	TCATCTTCTCAACTGGGTGACCTGGCGCATGTTCCGGCCATGCGAGACATCGCTGTG	700
Qy	142	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlav	162
Db	701	ACTCCAGCGTGGCGGATCTCGAGGCGCTTGAAGTACTTCATCTTGGCTTCTTGGCG	760
Qy	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysThrLeuGlyA	182
Db	761	TGGAGATGGTGGTGAAGATGGTGGCTTGGGCATCTTTGGGAAAAGTGTACTCTGGAG	820
Qy	182	spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTrpSerLeuA	202
Db	821	ACACTTGGAAACCGGCTTGAATTTTTCATCGTCACTCGCAGGAGTCTCGAGTACTCGCTGG	880
Qy	202	spLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
Db	881	ACCTGCAGAACGTCAGCTTCTCAGCTGTACGAGCAGTCCGTTGTCTCGACCCGCTCAGGG	940
Qy	222	laileAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProM	242
Db	941	CCATTAAACCGGGTGCCAGCATGGCGATCTTGTGTCAGTTGCTGTGTGATACGCTGCCCA	1000
Qy	242	etLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyV	262
Db	1001	TGCTGGGCAACGTCCTGCTGCTGCTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1060
Qy	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP	282
Db	1061	TCCAGCTGTGGGAGGGCTGCTTCGGAAACCGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1120
Qy	282	roLeuSerValAspLeuGluProTyTrpThrGlnThrGluAsnGluAspGluSerProPheI	302
Db	1121	CCCTGAGCGTGGACCTGGAGCGCTATTATCCNAGACAGAGACAGAGATGAGAGCCCTTCA	1180
Qy	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	1181	TCTGCTCCAGCCACGCGAGAACGGCATGGGTCTCTGCAGAAAGCGTCCCGCAGCGTGGCG	1240
Qy	322	lyGluGlyGlyGlyProProCysSerLeuAspTyThrGluThrTyThrAsnSerSerA	342
Db	1241	GGGACGGGGCGGTGGGCCCACTTGGCGTCTGGAGTATGAGGCTTACACAGCTTCCAGCA	1300

Qy	342	snThrThrCysValAsnTrpAsnGlnTrpTyThrAsnCysSerAlaGlyGluHisAsn	362
Db	1301	ACACCACTGTGTCAACTGGAACCACTACTACCACTACTGCTCAGCGGGGAGCACAACC	1360
Qy	362	roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyThrAlaTrpIleAlaIlePheGlnV	382
Db	1361	CCTTCAAGGGCGGCATCACTTTGACAACTATGGCTATGGCTGGATGCCATCTTCCAGG	1420
Qy	382	allIeThrLeuGluGlyTrpValAspIleMetTyPheValMetAspAlaHisSerPheT	402
Db	1421	TCATCAGCTGGAGGGCTGGTGCATCATGATCTTTGTGTGATGGATGCTCATCTCTCT	1480
Qy	402	yrAsnPheIleTyPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuC	422
Db	1481	ACAATTTTCATCTACTTCTCATCTCTCATCATCTGTTGGCTCTCTTCTCATGATCAACCTGT	1540
Qy	422	ysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	1541	GCCTGGTGGTATGGCCAGCAGTCTTCAGAGACCAAGCAGCGGAAAGCAGCTGATGC	1600
Qy	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1601	GGAGAGACGCTGTGGTCTCTTCCAAACCCAGCAGCTTGGCTGCTCTCTGAGCCCG	1660
Qy	462	lySerCysTyThrGluGluLeuLysTyThrLeuValTyThrIleLeuArgLysAlaAlaArgA	482
Db	1661	GCAGCTGTATGAGGAGTCTCAAGTACCTCTGGTGTACATCTTCTGTAAGCAGCCCGCA	1720
Qy	482	rgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1721	GGCTGGTCAAGTCTCTCGGGCAGCAGTGTGGGGTGGGGTGGCTGCTCAGCAGCCAGCAC	1780
Qy	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1781	CCCTCGGGGGCCAGGAGACCCAGCCAGCAGAGCTCTCTGCTCCACCCGCCCTAT	1840
Qy	522	erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis	542
Db	1841	CCGTCCACCACTGTGTGCACCACCACCACCACCACCACCACCACCACCACCACCACCACC	1900
Qy	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGAGAGGATGCCAATGGGTCCC	1960
Qy	562	rgArgLeuMetLeuProProSerProSerProSerProSerProSerProSerProSerPro	582
Db	1961	GCCGGCTCATGCTGCCACCACCTCGACGCTGCTCTCCGGGGCCCCCTCGTGGCG	2020
Qy	582	laGluSerValHisSerPheTyThrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTGTGTCACAGCTTCTACCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2080
Qy	602	laProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCTCATCTGAGGCATCCGCGCAGCATGTGGGCGAGGGAGGTGT	2140
Qy	622	yrProThrValHisThrSerProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCCCCGTGGCACACCGAGCCCTCCACCGGAGACGCTGGAAGGAGAGGAGGAGGAGGAGG	2200
Qy	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2201	TGGCTGCCAGCTTGGGGCCCCCAACCTCACAGCTCAACATCCCCACCGGGGCTTACA	2260
Qy	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGCAAGAGTCTGGAGACACAGAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2320
Qy	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrc	702
Db	2321	TCTCCAGCCCTTCTTGAAGCAGACAGTGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2380
Qy	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722

Db 2381 GTGCCCGGCGGCGGAGGAGTGGAGCTCGCGCAACCGTGAATGCTGACTCAGACA 2440
 Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis 742
 Db 2441 GCGAGGACATTTAGTTCACACAGGATGCCACAGAGACCTCCGGGACCCCCACA 2500
 Qy 742 erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
 Db 2501 GC---CGGCGGACACGAGACCTGGGCCAGATGACAGAGCCAGCTGTGTGCTGGCTTCT 2557
 Qy 762 rPargLeuLeuCysAspThrPheArgLysLeValAspSerLysTyrPheGlyArgGlyI 782
 Db 2558 GGAGGCTAATCTGTGACACCTTCGAAAGATTGTGGACAGCAAGTACTTGGCCGGGAA 2617
 Qy 782 leMetileAlaLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG 802
 Db 2618 TCATGATCGCATCTCTGGTCAACACACTCAGCATGGGCATCGAATACCAGAGAGCCCG 2677
 Qy 802 luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
 Db 2678 AGGAGCTTACCAAGCCCTAGAAATCAGCAACATCTCTTCCAGCCTCTTTGCCCTGG 2737
 Qy 822 luMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
 Db 2738 AGATGCTGCTGAAGCTGCTGTGTATGTGTCCTTGGCTACATCAAGAATCCCTACA 2797
 Qy 842 lePheAspGlyValIleValIleSerValTyrGluIleValGlnGlnGlyGlyG 862
 Db 2798 TCCTTCGATGGTGTCTATGTCGTATCATCGTGTGGGAGATCGTGGGCCAGCAGGGGGCG 2857
 Qy 862 lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP 882
 Db 2858 GCCTGTGCTGTCGCGACCTTCGCTGTATGCTGTGTGCTGAAGCTGGTGGCTTCTGTC 2917
 Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
 Db 2918 CGGCGCTGCAGCGGAGCTGTGTGTCTATGAAGACCATGAGCAAGCTGGCCACCTTCT 2977
 Qy 902 ysMetLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
 Db 2978 GCATGCTGCTTATGCTCTTCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3037
 Qy 922 ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL 942
 Db 3038 GCAAGATTTCCTCTGAGCGGATGGGACACCTTGGCCAGACCGGAAGAAATTTGACTCT 3097
 Qy 942 euLeuTyrAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAsnLysVal 962
 Db 3098 TGCTCTGGGCCATCTGCTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3157
 Qy 962 euTyrAsnGlyMetAlaSerThrSerSerTyrAlaLeuTyrPheIleAlaLeuMetT 982
 Db 3158 TCTAATAGTATGAGCTCCACGTCGCTCGTGGGCGGCTTTTATTTCAATGGCTTCAGA 3217
 Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnA 1002
 Db 3218 CCTTCGGCAACTACGCTGCTTCTTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTG 3277
 Qy 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
 Db 3278 CGGAGGAGATGCCAACAGTCCGAATCAGAGCCCGATTCTTCTTCTTCTTCTTCTTCT 3337
 Qy 1022 lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGluHisAlaGluLeuA 1042
 Db 3338 GTGATGGGACAGGAGAGTCTTGGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 3397
 Qy 1042 xgLySerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062
 Db 3398 GGAAGAGCTTGTGCGCTCTCTCATCTCCACAGCGGCCACACCCATGCTGCTGCCA 3457
 Qy 1062 ysSerSerSerThrGlyValGlyAlaLeuGlySerGlySerArgArgThrSerSers 1082

Db 3458 AGACACCAGCAGCGGCGCTGGGCGAGCGCTGGGCGCTGCTGCGCCGCGCACCGAGCA 3517
 Qy 1082 erGlySerAlaGluProGlyAlaAlaHisIleSgluMetLysCysProProSerAlaArgS 1102
 Db 3518 GCGGCTCGGAGAGCTTGGGCGGCGCC---CACAGATGAAGTCACTCCCGCCAGCGCCGCA 3574
 Qy 1102 erSerProHisSerProTyrPheSerAlaAlaSerSerTyrPheSerArgArgSerArgA 1122
 Db 3575 GCTCTCCGACACGCCCTCTGGAGCGCTGCAAGCAGCTGGACACGAGCGCTCCAGCGGA 3634
 Qy 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgSerL 1142
 Db 3635 ACAGCTCGGCGCTGACACCGCTGAAAGCGGAGAGCCCAAGTGGAGAGCGCGGCTCCC 3694
 Qy 1142 euLeuSerGlyGluGlyGlnIleSerGlnAspGluGluGluSerSerGluGluAspArgA 1162
 Db 3695 TGTGTCTGGGAGAGGCGCAGAGAGCCAGGATGAGAGGAGAGCTCAGAGAGAGCGGG 3754
 Qy 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers 1182
 Db 3755 CCAGCCTCGGCGGCTGACCATCCACAGCGGGTCCCTGGAGCGGAGGCCAAGAGTT 3814
 Qy 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
 Db 3815 CTTTGTACCTGCCACACACTGTCAGGTGCCAGGGCTGCATCGCATCTGCCAGTGGCCGAG 3874
 Qy 1202 erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
 Db 3875 GGTCTGCTTCTGAGCACCCAGGACTGCAATGCAAGTGGCTTCAAGGCGCTGCGCGGG 3934
 Qy 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeu 1241
 Db 3935 CCCTGCGGCTGATGACCCCGCTGATGGGAGTGCAGCGGATGACGCGGAGGCAACCTG 3993

RESULT 8
 US-10-377-139-8
 ; Sequence 8, Application US/10377139
 ; Publication NO. US20040175761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MacKinnon, Roderick
 ; APPLICANT: Jiang, Youxing
 ; APPLICANT: Lee MacKinnon, Alice
 ; APPLICANT: Ruta, Vanessa
 ; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
 ; TITLE OF INVENTION: Uses Thereof
 ; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
 ; CURRENT APPLICATION NUMBER: US/10/377,139
 ; CURRENT FILING DATE: 2003-03-01
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 6990
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-377-139-8

Alignment Scores:
 Pred. No.: 0 Length: 6990
 Score: 5432.50 Matches: 1234
 Percent Similarity: 62.21% Conservative: 241
 Best Local Similarity: 52.05% Mismatches: 514
 Query Match: 45.17% Indels: 387
 DB: 62 Gaps: 62

US-09-611-257A-24 (1-2287) x US-10-377-139-8 (1-6990)

Qy 12 ThrProLeuArgGlySerAlaArgProSerSerAspPro----- 25
 Db 16 TCCCGCGCTCTCTCATCTGAGCAGCCCGCCAGCGCTGAGCGAGTACACAGGAGCAG 75
 Qy 26 ProGlyProArgLeuAlaArgGlyTyrPheArgArgMetGluAlaProArgSer 45
 Db 76 CCGGAGCCCCGG----- 87

QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyValAlaGly 65
Db 88 -----AGCCCCCATCTCCCGCCAGGCTGGAGAGCTCTGGATGGAGCT----- 135
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 136 -----GATCCT-----CATGTCCCACAC 153
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 154 CCAAGACTGGCGCTATTGCTCTCTGCTCGACAGACACCACCGCCCGGAACTGG 213
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 214 TGCATCAAGATGGTGTCCACCCGCTGTTGAATGTGTACAGCATGCTGGTGTCTGCTG 273
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 274 AACTGCGTGACACTTGGCATGTATACAGCCGTGCGACGACATGACCTGCTCCGACCGC 333
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheAlaValGluMetVal 165
Db 334 TGAAGATCTCGAGGTCTTTGATGACTTCACTCTTTATCTTCTTGTCCATGGAGATGGT 393
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185
Db 394 CTCNAGATGTGGCCCTGGGGATTTTGGCAGNAGTGTCTACCTCGGGGACATGGNAC 453
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 454 CGCTGTGATTTCTCATCGTCAATGGCAGGATGTCGAGTACTCCCTGGACCTTCAGAAC 513
QY 206 ValSerPheSerAlaValAlaGlyThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 514 ATCAACCTGTGAGCATCCCGACCGCTGCGCTGCTGAGGCCCTCAAAGCCATCAACCGC 573
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 574 GTGCCAGATATGGGATCTCTGGTGAACCTGCTCTGACACACTGCCCATCTCTGGGGAAT 633
QY 246 ValLeuLeuLeuCysPhePheValPhePheGlyIleValGlyValGlnLeuTrp 265
Db 634 GTCTGTCTGTCTCTCTTGTCTTCTTCTATCTTGTGACATCATAGGTGTGACGCTGG 693
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 694 GCGGGCTGTGCGTAAACCGCTGCTTCTGAGGAGAACTTCAACATCAAGGGGATGTG 753
QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 754 GCCTTGGCCCCCATACTACCGAGCGGAGGATGATGATGATGCTCTCTCTCTCTCTG 813
QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 814 TCGGGCCACAATGGATAATGGGTGCGCATGATCCCGCTCAAGGAGCAG----- 867
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 868 ---GGCCGTGAGTGTCTGCTCAAGGACGACGTCTACGACTTTGGGGCGGGCGCCAG 924
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysAla 357
Db 925 GACCTCAATGCCAGCGCTCTGTGTCACTGGNACCGTTACTACAATGTGTGCGGACG 984
QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 985 GGCAGCCCAACCCCAAGGGTGCCATCAACTTTTGACAACATCGGTATGCTTGGATT 1044
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
Db 1045 GTCATCTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTAGTGTGAT 1104

QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1105 GCTCACTCTCTTACAACTTCATCTACTTATCATCTCTTATCATAGTGGCTCTCTTCTTC 1164
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1165 ATGATCAACCTGTGCTCGTTGTTCATAGCAGCCAGTTCTCGAGACCAAGAACCGGAG 1224
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1225 CACCGCTGATGTGGAGCAGCGCAGCGCTACTGTCC---TCCAGCAGGTGGCCAGC 1281
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1282 TAGCGCAGCTGGCGACTGCTACGAGGAGATCTTCAGTATGTCTGCCACATCTCTGCGC 1341
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1342 AAGGCCAAGCGCGCGCTTACGAGCGCTTACGAGCGCTCGAGCGCGCGCCAGGCCCTG 1401
QY 498 SerSerProValAlaAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1402 ---GGCCGAGCGCCCGCCCGCCCAACCTGGGCCC----- 1437
QY 518 HisArgLeuSerValHisHisLeuValHisHisHisHis----- 533
Db 1438 -----CACGCCAAGGAGCGCCCGCCACTTACCATGGGAAGACTAAG 1476
QY 534 -----HisHisTyrHisLeuGlyAsn-----GlyThrLeuArgValPro 547
Db 1477 GGTCAAGGAGATGAAGGAGACATCTCGGAAGCGCGCATTTGCCAGACTTTTGCATGGCCCT 1536
QY 548 ArgAlaSerPro-GluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeuPr 567
Db 1537 ---GCCTCCCTCGAATGATCACTCGGAGAGAGCTGTGCGCCGCAACATA---GCCCC 1590
QY 567 OProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa 585
Db 1591 CTGGATGCGAGCGCCCGACACCTCTGGTGCGCCCATCCCGCCACGC----- 1636
QY 585 lHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
Db 1637 -----TGCTTCCGATCCC 1650
QY 605 OArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa 625
Db 1651 GCAGTGGCTGTGTGTCAGCATGAGAGCGCGCGCGCTCGGCCCTGG----- 1702
QY 625 lHisThrSerProProGluIleLeuLysAspLysAlaLeuValAlaProSe 645
Db 1703 -----GCAGCACCGACTCGGCGCAGGAGGCTCGGCT----- 1735
QY 645 rProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHi 665
Db 1736 -CCGGAGCTCCGCTGGTGGC----- 1756
QY 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685
Db 1757 -----AGACGAGCGGATGGG----- 1774
QY 685 OYSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh 705
Db 1775 -----AC 1776
QY 705 rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVa 725
Db 1777 GGGCGCGGAGCAGCAGG----- 1795
QY 725 lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgAr 745
Db 1796 -----ACGAGCTCTCAGAACCTGGGAGGAGG-----AGGAGGAGGAG 1836
QY 745 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuI 765

1837	Db	GAGCAGCGCGATGGCGGGTCTGGCTG-TGCGGGGATGTG-----TGCGGGGAGAC	1886
765	QY	eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl	785
1887	Db	GCAGGCAAGCTCGCGGGCATCTGTGACAGCAAGTACTTCAACGGGGGATCATGATGGC	1946
785	QY	alleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluInProGluGluLeuTh	805
1947	Db	CATCTTGGTCAACACCGTCAGCATGGCATCGAGCACCAGCAGCAGCGGAGGAGCTGAC	2006
805	QY	rAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLe	825
2007	Db	CAACATCTCGAGATCTGCAATGTGTCTCACAGCATGTTTGGCCCTCGAGATGCTCT	2066
825	QY	uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl	845
2067	Db	GAAGCTGGCTGCATTGGGCTCTTCGACTACTCTGGTACCCCTACCAATCTTCACAG	2126
845	QY	yValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerVa	865
2127	Db	CATCATTTGTCATCATCAGCATCTGGAGATCGTGGGGCAGCGGACGGTGGGCTGTCTG	2186
865	QY	lleuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGl	885
2187	Db	GCTCGGAGACCTTCGGCTGTCTGGCTGTCTGAACTGGTGGCTTTCATGCTGCCCTGGC	2246
885	QY	nArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe	905
2247	Db	GCGCCAGCTCGTGGTGTCTCATGAAGACCATGGACAACGTGGCCACCTTCTGCATGCTG	2306
905	QY	uMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAl	925
2307	Db	CATGCTCTTTCATCTTCACTTCAGACTCTTGGATGTCATATTTTGGCTGCAAGTTCCAG	2366
925	QY	aserGluuArgsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr	944
2367	Db	CCTCCGCACGGACACTGGAGACACGGTGGCCGACAGGAAGAACTTCGACTCCCTGTGTG	2426
944	QY	pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTrAs	964
2427	Db	GGCCATCGTCACTGTGTTCAGATCTTCACCCAGGAGGACTGGAACGTGCTTCTACAA	2486
964	QY	nGlyMetAlaSerThrSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl	984
2487	Db	TGGCATGGCCCTCCACTTCTCCCTGGGCTCCCTCTACTTTGTGCGCCCTCATGACCTTCG	2546
984	QY	yAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGl	1004
2547	Db	CNACTATGTGCTTCAACTGCTGGTGGCCATCCTGTGGAGGCTTCAGGCGGAGGG	2606
1004	QY	yAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal-----1020	1020
2607	Db	TGAGCCCAATCGCTCTTACTCGGACGAGGACAGAGCTCATCCACATAGAGAGTTTGA	2666
1021	QY	-----AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAl	1034
2667	Db	TAAGCTCCAGGAAGCGCTGGACAGCAGCGGAGATCCCAAG-----CTCTGCCCAATCCC	2720
1034	QY	aLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThr--	1053
2721	Db	CATGACCCCAATGGGACCTGGACCCCAAGTCTC-----CCATGGGTGGGCACCTAGG	2774
1054	QY	-----AlaAlaThrProMetSerHisProLysSerSerThrGlyValGlyGl	1070
2775	Db	TCCTGTGGGCTGCGGACCTGGC-----CCCCGACTCTCACTGACGCGGACCCCAT	2828
1070	QY	uAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl	1090
2829	Db	GCTGGTGGCCCTGGGCTCCCAAGAGAGAGAGTGTCTCTCTA-----GGAGAGAT	2879
1090	QY	aHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAl	1110

[illegible]

Qy	1449	ePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAl	1469
Db	3996	CTACCACCTGTCTGGCGCTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGC	4055
Qy	1469	aSerTyrArgTrpValAlaArgHisIysTyrAsnPheAspAsnLeuGlyClnAlaIeuMetSe	1489
Db	4056	CAACTACCGCTGGGTTCATCACAATACAACTTCGCAACCTGGCGCAGGCTCTGATGTC	4115
Qy	1489	rLeuPheValLeuAlaSerLysAspGlyTTrpValAspIleMetTyrAspGlyLeuAspAl	1509
Db	4116	CCTCTTTGTCTCGCATCCCAAGGATGTTGGTGGAACATCATGTACAAATGGACTGGATGC	4175
Qy	1509	aValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIl	1529
Db	4176	TGTTGTCTGGACGAGCAGCCTGTGACCAACACCAACCCCTGGATGCTGCTGACTTCAT	4235
Qy	1529	eSerPheLeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValValValGl	1549
Db	4236	CTCCTTCTCTGCTCATGCTACGCTCTTTTGTGCTCAACATGTTTGTGGGTGTCTGTGTGGA	4295
Qy	1549	uAsnPheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLy	1569
Db	4296	GAACTTCACAAGTCCGCGCAGCACACGAGGCTGAAGAGCACCGCGCGTGGAGGAA	4355
Qy	1569	sArgLeuArgIeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGl	1589
Db	4356	CGCGCTCGCGCGCTGGAGAAGAAGCCCGG-----AAGGCCCA	4394
Qy	1589	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysCysTh	1609
Db	4395	CGCGCTGCCTCATATGCCACTATTGTCAACCCGGCTGCTCATCCACTCCATGTGCAC	4454
Qy	1609	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl	1629
Db	4455	CAGCCACTACCTGACATCTTCATCACTTCATCATCTGCCTCAACGTGTGCACCATGTC	4514
Qy	1629	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIl	1649
Db	4515	CCTGGAGCACTACAAATCAGCCCAACGCTCCCTGGAGACGCCCTCAAGTACTGCAACTAT	4574
Qy	1649	ePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgAr	1669
Db	4575	GTTCACCACCTGCTTTGTCTGGAGGCTGTGCTGAAGCTGGTGCACTTTGGTCTGAGCGC	4634
Qy	1669	gPhePheClnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGl	1689
Db	4635	CTTCTTCAAGACCGATGGAAACCAAGCTGGACCTCGCCCATTTGTCTACTGCATGCATGGG	4694
Qy	1689	yIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleAr	1709
Db	4695	CATCACCTTGAGGAGATCGAGATCAATCGCGCCCTGCCCATCAATCCCACCATCATCCG	4754
Qy	1709	gIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMe	1729
Db	4755	CATCATGAGGGTTCTCGCATTCGCCGAGTCTGAAGCTGTGTAAGATGGCCACGAGAA	4814
Qy	1729	tArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1749
Db	4815	CGCGGCCCTCTGGACACGGTGTGCAAGCTTTGCCCGAGGTGGGCAACCTGGGCGCTCCT	4874
Qy	1749	uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGl	1769
Db	4875	CTTCATGCTGCTCTTCTTCATCTATGCTGCTCTCGGGGTGGAGCTCTTTGGGAAGCTGGT	4934
Qy	1769	uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGl	1789
Db	4935	CTGCAACGACGAGAACCCTGCGAGGGCATGACGCGGCATGCCACCTTCGAGAACTTCGG	4994
Qy	1789	yMetAlaPheLeuThrIeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy	1809
Db	4995	CATGGCTTCTCTCACTCTTCAGGTTCTCAACGGGTGACAACTGGAACCGGATCATGAA	5054

Qy	1809	sAspProSerArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il	1826
Db	5055	GGACACGCTGCGGACTGCACCCACGACGAGCGCGACTGCCTGCAGCAGCTGCAGCATTTGT	5114
Qy	1826	eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1846
Db	5115	GTCCGCCCTGTACTTCTGTGAGCTTCGTGCTCACCGCGAGTTCTGTCTCATCAACGTGGT	5174
Qy	1846	lIleAlaValLeuMetIlyHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGl	1866
Db	5175	GGTGGCTGTCTCATGAAGCACCTGGACGACGACCAACAGGAGCGCGAGGAGCAGCGCA	5234
Qy	1866	uLeuGluAlaGluLeuGluMet----LysThrLeuSerProGlnProHisSerPr	1885
Db	5235	GATGGATCGCGAGCTCAGCTGGAGATGGCCCATGGCTTGGGCCCTTGGCCCGAGGCTGCC	5294
Qy	1885	oLeuGlySerProPheLeuTrpPro-----GlyValGluGlyValAsnSe	1900
Db	5295	TACCGGCTCCCGGGGCC--CTGGCCGAGGGCCGGAGGGCGCGCGGGGGCGCA	5351
Qy	1900	rThrAsp-----SerProLysProGlyAlaPro-----	1909
Db	5352	CACGAGGGCGGCTTGGCCGGCGCTGCTACTCGCCTGC-CCAGGAGAACCTGTGGCTGG	5410
Qy	1910	---HisThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMe	1928
Db	5411	ACAGCGTCTCTTTAATCATCAAGGACTCCTTGGAGG---GGAGCTGACCAT-----	5459
Qy	1928	tValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLy	1948
Db	5460	-----CATCGAACACTGTGGCGCTCCATCTTCCACCACTACTCTCTCGCTGCCGGCT	5512
Qy	1948	sSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySe	1968
Db	5513	GCAGAGAGTGTC-----CCACGACAA-----	5534
Qy	1968	rThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe	1988
Db	5535	---GCAAGAGGTGCAGCTGGCTGAGACGGAGGCTTCTCCTGAACTCAGACAGGTCTCT	5590
Qy	1988	rIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAs	2008
Db	5591	CGTCCATCTCTGGTGAGCAGCCTGAGCTCTCGAGGA-----	5627
Qy	2008	pValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPr	2028
Db	5628	-----CCCCACGCTGCCACCTGG-----CGCAAGACACA	5659
Qy	2028	oPro-----ProGlyArgSerProLe-----	2035
Db	5660	GCAAGGGTGAGCTGCACCCACCTGAGGCCATCGTGTGGGAGACCTGGGCGAATGCTCT	5719
Qy	2035	uAlaGluArgProLeuArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGl	2055
Db	5720	TCCCTTGT-CCCTACGGCGCTCTCCCGGATCCAGAGAACTTCTCTGT---GTGAGATG	5775
Qy	2055	yLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrAr	2075
Db	5776	GAGAGATCCCAT-----TCACCCCTCTCCGGTCTGGCTGCAACATGACA--	5821
Qy	2075	gSerSerSerPheTrpGlyGlySerIleGlnValGlnArgSerGlyIleGlnSe	2095
Db	5821	-----	5821
Qy	2095	rLysValSerIlyHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAl	2115
Db	5822	---GCAGTCAAGCACCCCAAGTCCCTTCTCC-----	5851
Qy	2115	aLysAspProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe	2135
Db	5852	CGATGCTCCAGCC-----CTCTC	5871
Qy	2135	rGlyAspLeuLeuProSerSerGlnGluGluProLeuPhePro-----ArgAspLeuLy	2153

Qy 398 AlaHisSerPheTyrAsnPhelIleTyrPheIleLeuLeuIleValGlySerPhePhe 417
Db 1296 GCTCCTCTTACAACTTCACTACTTCTCTCTTATCATAGTGGCTCTTCTTC 1355
Qy 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGCTGTGTATAGCAGCACCGTTCGAGAGACCAACGCGAG 1415
Qy 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACGGCTGTATCTGGAGCAGCGCAGCTACCTGCTCC---TCCAGCAGGGTGGCCAGC 1472
Qy 458 PheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TAGCCGAGCCTGGCGACTGCTACGAGAGATCTTCAGTATGCTCCCATCTCTCGCG 1532
Qy 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGCCCAAGCGC-----CGCGCCCTGGGCTCTACCGAGCGCCTGCAG 1574
Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
Qy 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisTyr 537
Db 1578 ---CGCGCCAGCGCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGCGCCCGCCCAAACTGGGCCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyA-gThrValGly 617
Db 1644 CGGCACCTACCAGCTGTGCGCGCAATAGCCCTCGATGCG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGTGCAG-----CCATCCCGCCACGCTGGCTTCC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCCCTTGTGCAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGCAGCGCGCGCGCTCGGGCTGGGCGAGCACCGACTCGGGCCAGGAGGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCGCTGGTGGCGAGGAGCGGCG----- 1853
Qy 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACGGGCGC-----CGGAGCAGCGAGGACCGAGCCTCTCAGAA 1898
Qy 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG 1940
Qy 757 SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp 774

Db 1941 GTCTGGCTGTGCGGGATGTGTGCGGAGACGCGAGCCAAAGCTGCGCGCATCTGTGGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATATGGCCATCTCTGTGTCAACACCGTCAGCATGGGC 2060
Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATGAGCACCACGAGCAGCGCGAGGAGTGACCAACATCTCTGGAGATCTGCATGTGGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPheGly 834
Db 2121 TTCACGACGATGTTTCCCTGGAGATGATCTCAAGCTGGCTGCATTTGGGCTCTTCGAC 2180
Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleValIleSerValTrpGlu 854
Db 2181 TACCTCGTAAACCCCTACAACTTCGACAGCATCATTTCTCATCATCATCTGGGAG 2240
Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATGTGGGCGAGCGGAGCGGTGGGTGTGCTGGGACCTTCGGCTGCTGGCGGTG 2300
Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGTGTGCGCTTCATGCTGCTGCGCGCGCAGCTCGTGTGTCTCATGAAGACC 2360
Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGGACAACGTGGCCACTTCTCATGCTGCTCATGCTCTTCTTCTTCTTCTTCTTCTTCT 2420
Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTGGGATGATATTTTGGTGCAGTTGCTGCTCGCAGGACACTGGAGACACCGGTG 2480
Qy 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGTCACTGTGTTCCAGATCCTC 2540
Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCAGGAGACTGGAAACGCTGTTCTTCTACAATGGCATGGCTCCCACTTCTCCCTGGGCC 2600
Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 993
Db 2601 TCCTCTACTTTGTGCGCTCATGACTTCGGCAACTATGTGTCTTCACTTCACTTCTGCTG 2660
Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTGTGTGGAGGCTTCCAGCGGAGGGTGAGCCCAATCGCTCTACTCGGACGAG 2720
Qy 1014 AspPheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGACTCTCAACATAGAGAGTGTGTAAGCTCCAGGAAGCCCTGGACAGCAGC 2780
Qy 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTTCCCCATCCCATGCCCAATGGGCACTGGACACCCC 2834
Qy 1044 SerLeuLeuProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGCACCTAGGTCTCTGGGCTGGGGACCTGCC--- 2885
Qy 1060 HisProLysSerSerSerThrGlyValGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCCGACTCTCACTGACCGGACCCCATGCTGTGGTGGCTCCCGGAGCAGC 2942
Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGTATGTCTCTA-----GGGAGATGAGTATGACCGCGCTCCCTGTCTCAGC 2993
Qy 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119

2994	TCCCGAGCTCTCTACTACGGGCCATGGGGCCGACGGCGGCTGTGGCCAGCGCTGCCTCC	3053
1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg	1139
3054	AGCTGGAAC-----AGCTCAAGCAACAAGCCGCTCGCGCGAGCAT	3095
1140	ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu	1158
3096	GAGTCCCTGCTCTCTCGGAGCGCGCGCGCGCTGTGCGAGTTCGCCGCGAC	3155
1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
3156	GAGGGCCCGCGCGCGCACCCCTGCACACCCACCGCCACCATTCATCAGCGG	3215
1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
3216	CCCATCTGTGGCAGACCGCCACCGCCGAGCGCTGTCCCTGCACAACAGGGAC	3275
1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1203
3276	TGGTGGACCTGCCGAGCTGGTGGCGCGGTGGCGGCCACCCCGGGCGCGCTGGAG	3335
1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
3336	CGCGCAGCCCGCGCCCGCGCATGAGGACTGCAATGGCAGGATGCCACG-----ATC	3389
1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
3390	GCCAAAGACGTCTTCCAAAGATGGGGCCCGGGGATCGCGGGAGGATGAGGAGAA	3449
1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
3450	ATCGACTACACCTGTCTTCCGCGTCCGCAAGATGATCGACGCTCTATAAGCCGCACTGG	3509
1259	CysArgGluArgSerThrProSerAlaTyrIlePheProGlnSerArgPheArgLeu	1278
3510	TGCGAGTCCGCGAAGACTGGTGTCTACTCTCTCCGAGAACAGGTTCCTGGGTC	3569
1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298
3570	CTGTGTGAGACCATTAATGCCCAACAACTCTTCGACTACGCTCTCTGGCCTTCATCTTT	3629
1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
3630	CTCAACTGCATCACCATCGCCCTGGAGCGCCCTCAGATCGAGCCGCGACACCGAACGC	3689
1319	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
3690	ATCTTTCTACCGTGTCCAACTACATCTTCACGGCCATCTTCGTGGCGGAGATGACATTG	3749
1339	LysValValAlaLeuGlyTyrCysPheGlyGlnGlnAlaTyrLeuArgSerSerTrpAsn	1358
3750	AAGTAGTCTCGCTGGCGCTGTACTTCGGGGAGCAGACGCTACCTACGCACAGCTGGAAC	3809
1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
3810	GTGCTGGATGGCTTCTTGTCTTCGTGTCAATCATCGACATCGTGTGTCTCTGGCGCTCA	3869
1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
3870	GCCGGGGAGCCAAAGATCTTGGGGGTCTCTCGAGTCTTGGCGCTCTCTGCGCACCTACGC	3929
1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
3930	CCCTCGCTGTTCATCAGCCGGCGCCGGCGCTGAAGCTGGTGGGGAGACATCATCTCC	3989
1419	SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly	1438
3990	TCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGTCTCTCTTCATCATCTTTGGC	4049
1439	IleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAspThrArg	1458
4050	ATCTCGGAGTGCAGCTCTTCAAGGGCAAGTCTTACCACTGTCTGGGCGTGACACCCGC	4109

1459	AsnIleThrAsnIlySerAspCysAlaGluAlaSerTyrAtqTrrpValArgHislysvTyr	1470	AsnIleThrAsnIlySerAspCysAlaGluAlaSerTyrAtqTrrpValArgHislysvTyr
4110	AAATCACCACCAACCTCGGACGTGCATGCCGCCCACTACCGCTGGGTTCATCACAATATAC	4169	AAATCACCACCAACCTCGGACGTGCATGCCGCCCACTACCGCTGGGTTCATCACAATATAC
1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerIlyAspGly	1498	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerIlyAspGly
4170	AACTTCGACAACTGGGCCAGGCTCTGATGTCCCTCTTTGTCTGGCATCCAAAGATGGT	4229	AACTTCGACAACTGGGCCAGGCTCTGATGTCCCTCTTTGTCTGGCATCCAAAGATGGT
1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet
4230	TGGGTGAACATCATGTACAAATGGACTGGATGCTTGTCTGGACACAGCGCTGGACC	4289	TGGGTGAACATCATGTACAAATGGACTGGATGCTTGTCTGGACACAGCGCTGGACC
1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe
4290	AACCAACACCCCTGGATGTCTGTACTTCACTCTCTCTCTGCTCATCGTCAGCTCTTT	4349	AACCAACACCCCTGGATGTCTGTACTTCACTCTCTCTCTGCTCATCGTCAGCTCTTT
1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisIlyCysArgGlnHisGln	1558	ValLeuAsnMetPheValGlyValValValGluAsnPheHisIlyCysArgGlnHisGln
4350	GTGCTCAACATGTTTGTGGTGTCTGGTGGAGAACTTCACAAAGTGCAGCAGACACAG	4409	GTGCTCAACATGTTTGTGGTGTCTGGTGGAGAACTTCACAAAGTGCAGCAGACACAG
1559	GluGluGluGluAlaArgArgArgGluGluIlyArgLeuArgArgLeuGluIlyIlyAsq	1578	GluGluGluGluAlaArgArgArgGluGluIlyArgLeuArgArgLeuGluIlyIlyAsq
4410	GAGGCTGAAGAGCAGCGCGCTGTAGGAGAACGGCTCGGGCCCTGGAGAAAGAGCGC	4469	GAGGCTGAAGAGCAGCGCGCTGTAGGAGAACGGCTCGGGCCCTGGAGAAAGAGCGC
1579	ArgSerIlyGluIlyGlnMetAlaGluAlaGlnCysIlyAspProTyrTyrSerAspTyrSer	1598	ArgSerIlyGluIlyGlnMetAlaGluAlaGlnCysIlyAspProTyrTyrSerAspTyrSer
4470	CGG-----AAGGCCACAGCGCTGCCCTACTATGCCACTATTGT	4508	CGG-----AAGGCCACAGCGCTGCCCTACTATGCCACTATTGT
1599	ArgPheArgIleuLeuValHisIleLeuCysThrSerHisTyrIleuAspLeuPheIleThr	1618	ArgPheArgIleuLeuValHisIleLeuCysThrSerHisTyrIleuAspLeuPheIleThr
4509	CACACCCGGTGTCTATCCACTCCATCGACGACGACCTACTCTGGACATCTTTCATCACC	4568	CACACCCGGTGTCTATCCACTCCATCGACGACGACCTACTCTGGACATCTTTCATCACC
1619	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1638	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle
4569	TTCATCATCTGCCCTCAACGTGGTTCACCATGTCTCTGGAGCAGCTACAATCAGCCACGTCC	4628	TTCATCATCTGCCCTCAACGTGGTTCACCATGTCTCTGGAGCAGCTACAATCAGCCACGTCC
1639	LeuAspGluAlaLeuIlyIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658	LeuAspGluAlaLeuIlyIleCysAsnTyrIlePheThrValIlePheValPheGluSer
4629	CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTACCACACTCTCTTGTGTGGAGGCT	4688	CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTTACCACACTCTCTTGTGTGGAGGCT
1659	ValPheIlyLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrrpAsnGlnLeu	1678	ValPheIlyLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrrpAsnGlnLeu
4689	GTGCTGAAGCTGGGGCATTTGGTCTGAGCGCGCTCTTCAAGGACCGATGGAAACCAAGCTG	4748	GTGCTGAAGCTGGGGCATTTGGTCTGAGCGCGCTCTTCAAGGACCGATGGAAACCAAGCTG
1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn
4749	GACCTGGCCATTGGCTACTGTCACTATGGGCATCACCCCTGGAGGAGATCGAGATCAAT	4808	GACCTGGCCATTGGCTACTGTCACTATGGGCATCACCCCTGGAGGAGATCGAGATCAAT
1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValIleuArgIleAlaArg	1718	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValIleuArgIleAlaArg
4809	CGCGCCCTGCCCATCAATCCACCATCATCGCATATGAGGGTTCGCGCATTTGCCCGGA	4868	CGCGCCCTGCCCATCAATCCACCATCATCGCATATGAGGGTTCGCGCATTTGCCCGGA
1719	ValLeuIlyLeuLeuIlyMetAlaValIlyMetArgAlaLeuLeuHisThrValMetGln	1738	ValLeuIlyLeuLeuIlyMetAlaValIlyMetArgAlaLeuLeuHisThrValMetGln
4869	GTGCTGAAGCTTTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACGGTGTGCAA	4928	GTGCTGAAGCTTTGAAGATGGCCACAGGAATGCGGGCCCTGCTGGACACGGTGTGCAA
1739	AlaLeuProGlnValGlyAsnLeuLeuPheMetIleuPhePheIlePheAla	1758	AlaLeuProGlnValGlyAsnLeuLeuPheMetIleuPhePheIlePheAla
4929	GCTTTGCCCCAGGTGGGCAACCTGGGCTCTCTTTCATGTGCTCTTCTTCATCTATGCT	4988	GCTTTGCCCCAGGTGGGCAACCTGGGCTCTCTTTCATGTGCTCTTCTTCATCTATGCT
1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly
4989	GCTCTCGGGGTGGAGCTCTTTGGGAAGCTGTGCTGCACACGACGAGAACCTGGCAGGGC	5048	GCTCTCGGGGTGGAGCTCTTTGGGAAGCTGTGCTGCACACGACGAGAACCTGGCAGGGC
1779	LeuIlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798	LeuIlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal
5049	ATGACCCGGCATGCCACCTTCGAGAACTTCGGCATGCGCTCTCTTCACACTCTTCCAGTCT	5108	ATGACCCGGCATGCCACCTTCGAGAACTTCGGCATGCGCTCTCTTCACACTCTTCCAGTCT
1799	SerThrGlyAspAsnTrpAsnGlyIleMetIlyAspProSerArgAspCys---AspGln	1817	SerThrGlyAspAsnTrpAsnGlyIleMetIlyAspProSerArgAspCys---AspGln
5109	TCCACGGGTGCAACTGGAACGGGATCATGAAGACACGCTGCGGGACTCACCCACGAC	5168	TCCACGGGTGCAACTGGAACGGGATCATGAAGACACGCTGCGGGACTCACCCACGAC

QY	66	AlaGlySerThrGluLeuAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr	85	MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu	437
Db	327	-----GATCCT	344	ATGATCAACCTGTGCTCTGTGTAGCGACCCAGTTCTCGAGACCAAGACGCGAG	1415
QY	86	ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTyr	105	438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer	457
Db	345	CCAGACTCGCGCTATTCCTCTCTCTGCTGCGACAGACCACCGCCCGGAACCTGG	404	1416 CACCGCTGATGTCGAGCAGCGCGCTACCTGTCTCCAGCAGCGTGGCCAGC	1472
QY	106	CysLeuArgThrValCysAsnProTyrPheGluArgValSerMetLeuValIleLeuLeu	125	458 PheSerGluProGlySerCysTyrGluGluLeuLeuLeuValTyrLeuValTyrIleLeuArg	477
Db	405	TGCATCAAGATGTGTGCAACCGTGGTTGAATGTGTGATGTCAGATCTGGTATCTGCTG	464	1473 TAGCGCAGCTGCGACTGCTACGAGGAGATCTCCAGTATGTCTGCCACATCTCTGCGC	1532
QY	126	AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145	478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	497
Db	465	AACCTGGTGACATTCGGCATGTACACCGCTGGAGCAGATGGACTGCTGCTGCCACCGC	524	1533 AAGCCCAAGCGC-----CGCGCTGGCTCTACCGAGCCCTGSCAG	1574
QY	146	CysArgIleLeuGlnAlaPheAspPheIlePheAlaPheAlaValGluMetVal	165	498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer	517
Db	525	TGCAAGATCTCGAGCTTTGATGACTTTCATCTTATCTTCTTGGCCATGGAGATGGTG	584	1575 AGC-----1577	
QY	166	ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn	185	518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisTyr	537
Db	585	CTCAAGATGTGGCCCTGGGGATTTTGGCAAGATGCTTACTCTCGGGACACATGGGAAC	644	1578 ---CGGCGCAGGCGCTG-----1592	
QY	186	ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn	205	538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluLeuGlnAspArgAsp	557
Db	645	CGCCTGGATTTCTTCATCGTCATGGCAGGGATGTCGAGTACTCTCCCTGGACCTTCAGAAC	704	1593 -----GGCCCGGAG-----1601	
QY	206	ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg	225	558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly	577
Db	705	ATCAACCTGTGAGCATCCGACCGCTGGCGTCTGAGGCCCTCAAGGCCATCAACCGC	764	1602 -----GCCCCGCCCCCGCAACCTGGGCCC-----1628	
QY	226	ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn	245	578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
Db	765	GTGCCAGTAGTGGCGATCTGTGTAACCTGCTCTGGACACACTGCCCATGTCTGGGAAT	824	1629 -----CACGCCAAG-----GAGCCC1643	
QY	246	ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp	265	598 ValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGly	617
Db	825	GTCTGTCTGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG	884	1644 CGGCACCTACGACTGTGCCCAACATAGCCCCCTGTGATGCG-----1685	
QY	266	AlaGlyLeuLeuArgAsnArgCysPheLeuProGluLeuPheSerLeuProLeuSerVal	285	618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys	637
Db	885	CGCGGCTGCTGCGTAACCGTGTCTCTGAGGAGAACTTCACCAAGGGGATGTG	944	1686 -----ACGCCCCACACC-----1697	
QY	286	AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln	305	638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	657
Db	945	GCTTTGCCCCATACCTACCGCGGAGGAGATGATGAGATGCCCTTTCATCTGCTCCCTG	1004	1698 ---CTGGTGCAG-----CCCATCCCGCCACGCTGGCTTCC-----1730	
QY	306	ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly	325	658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys---	676
Db	1005	TCGGCGCAATGGGATATGGTGGTGCATGAGATCCCCCGCTCAAGGACGAG-----	1058	1731 -----GATCCCGCCAGCTGCTGCTGCCAG1757	
QY	326	GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer	339	677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	696
Db	1059	GGCCGTGAGTGTGCTGTGTCACAGCAGCGCTACGACTTTGGGGCGGGCGCCAG	1115	1758 CATGAGCAGCGCGCGGCGCTCGGCGCTGGGACACCGACTCGGGCCAGAGGGCTCG	1817
QY	340	SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrThrAsnCysSerAla	357	697 AspSerCysProTyrCysAlaargThrGlyAlaGlyGluProGluSerAlaAspHisVal	716
Db	1116	GACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGTTACTACATGTGTGCGGACG	1175	1818 GGCTCC-----GGGAGCTCCGCTGGTGGGAGGACGAGCGG-----1853	
QY	358	GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle	377	717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	736
Db	1176	GGCAGCGCCCAACCCCAAGGGTGCCATCACTTTGACACATCGTTATGTCTGGATT	1235	1854 -----GATGGGACCGGGCC-----CGGAGCAGCAGGACGAGCCCTCTCAGAA1898	
QY	378	AlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp	397	737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer	756
Db	1236	GTCACTTCCAGGTATCACTCTGGAAGGCTGGGTGGAGATCATGTACTACGTATGATG	1295	1899 CTGGGAAGGAGGAGGAGGAGGAGGAGGAGC-----CGGATGGGCG1940	
QY	398	AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe	417	757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp	774
Db	1296	GCTCACTCTCTACAACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC	1355	1941 GTCTGGCTGTGGGGATGTGTGGGGAGACCGGAGCCAAAGCTGCGCGCATCTGTGAC	2000
QY				775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly	794

Db 6010 TTGGCGCTG-CAGGGCTCTCGGCGATCT-----CTGCGGTCAACAAAGGTCAACTGT- 6059
Qy 2184 Leu-----ApsSerGlySerClnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCTCCGGCAGGCCAGCGGAGGACACGTCGCTGGAGCGCAGCCCGCAGCAG-CTC 6118
Qy 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer 2219
Db 6119 CGCGGGCAGCTCGAGACCAGCTCGAGGACAGCTGACCTGACGCGACGACGCCCGCGCG 6178
Qy 2220 lleserleApsProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGCCCTGGGCGCGCGCGCTGCTCCAGGACCCCGCGC 6217
Qy 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCTGTGCCCCCGCTCGCCCGCGCTGAGCTCGCGCGCGCGCTCTTCAGCCT 6277
Qy 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTCGGGCGGATCAGCCAGCAGCGGGGCTCCACCAGCCCGGCTG 6337

RESULT 11

US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 9 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

Qy 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCGCGCTCTCATCTGAGCAGCAGCCCGCGCTGAGCGAGGTCAACACGAGCAG 266
Qy 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
Qy 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGGCTGAGGAGGCTCTGGATGAGCT----- 326
Qy 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTy 85
Db 327 -----CATGCTCT-----CATGCTCCACAC 344

Qy 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGGGCTATTGCTTCTTGGCTGGACAGCACCAGCCCGGAACTGG 404
Qy 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValLeuLeu 125
Db 405 TGCATCAAGATGGTGTGCAACCGCTGTTGAATGTGTGACGATGCTGGTGTCTGCTG 464
Qy 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspLeuAlaCysAspSerClnArg 145
Db 465 AACTGCTGACACTTGGCATGTATCCAGCGTGCACGACATGGACTGCTCTCCGACCGC 524
Qy 146 CysArgileLeuGlnAlaPheAspPheilePheAlaPhePheAlaValGluMetVal 165
Db 525 TGCAGATCTCGAGGCTTTGATGACTTCATCTTTATCTTTTGGCATGGAGATGGTG 584
Qy 166 ValLysMetValAlaLeuGlyilePheGlyLysLysCysTyrLeuGlyAspThrPAsn 185
Db 585 CTCAGATGTGGCCCTGGGGATTTTGGCAAGAGTGTACCTCGGGGACACATGGAAC 644
Qy 186 ArgLeuAspPhePheileValileAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCTGGATTTCTCATGTCATGGCAGGATGGTCCAGTACTCCCTGGACCTTCAGAAC 704
Qy 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaileAsnArg 225
Db 705 ATCAACCTGTACGATCCCGACCGTGGCGTCTGAGGCCCTCAAGCCATCAACCGC 764
Qy 226 ValProSerMetArgileLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGGGATCTCTGGTGAACCTGCTCTGAGACACACTGCCCATCTGGGAAT 824
Qy 246 ValLeuLeuLeuCysPheValPhePheilePheGlyileValGlyValGlnLeuTrp 265
Db 825 GTCTGTCTGCTCTCTTCTTGTCTTCTTCTTGTGTCATCATGAGTGTGTCAGCTCTGG 884
Qy 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGGCTCTGGGTAAACCGCTGCTCTGAGGAGAACCTTACCATACAGGGGATGTG 944
Qy 286 AspleuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheileCysSerGln 305
Db 945 GCCTTGCCCCCATACTACACGCGGAGGAGATGATGAGATGCCCTTTCATCTGCTCCTG 1004
Qy 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
Db 1005 TCGGGCGACAATGGGATAATGGGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
Qy 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ----GGCGTGAGTGTGCTGCTTCCAGGACGAGCTGTACGACTTTGGGGGGGGCGCAG 1115
Qy 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGTTACTACAAATGTGTGCGGACG 1175
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Qy 378 AlailePheGlnValileThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp 397
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QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisLeuValHisHisHisHisHisHisHisHisHis 537
Db 1578 ---CGGCCGACGCCCTG----- 1592
QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
QY 558 AlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGGCCCGCCCAACTGGGCC----- 1628
QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CAGCCCAAG-----GAGCCC 1643
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Db 1644 CGGCACCTACAGCTGTGCCCGCAACATAGCCCCCTGGATGCG----- 1685
QY 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 -----AGCCCCACAC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnLeuPro 657
Db 1698 ---CTGGTGCGAG-----CCATCCCGCCAGCGTGGCTCC----- 1730
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrClnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCCCTGTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
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QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
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QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
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QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
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QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGAGCTCATCCACATAGAGTTGATAGCTCCAGGAAGCCTGGACAGCAGC 2780
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QY 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
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QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCTATCTCTA-----GGGAGGATGAGCTATACCCAGCGCTCCCTGTCCAGC 2993
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCCGAGCTCTTACTACCGGCCATGGGCCCGCGCGCTGGGCCAGCCGCTGCTCC 3053
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DB 405 TGCATCAAGATGGTGTGCAACCGTGGTGTGATGTGTGATGCTGCTGCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
DB 465 AACTGCGTGACATTGCGATGTACACCGCTGGCAGACATGAGTGCCTCGGACCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePheAlaValGluMetVal 165
DB 525 TGCAGATCTCGCAGGCTTTGATGACTTCATCTTTATCTTTGTCATGGAGATGGTG 584
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DB 585 CTCAGATGGTGGCCCTGGGGATTTTGGCAAGAAGTGTACCTCGGGGACACATGGAAC 644
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QY 326 GlyGlyProProCysSerLeu- 339
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QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
DB 1575 AGC- 1577
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DB 1629 - 1643
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DB 1731 - 1757
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DB 1854 -GATGGGACGGGGCC- 1898
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QY 757 SerValLeuAla- 774
DB 1941 GTCTGCTGTGCGGATGTGTGCGGAGACGCGAGCCCAAGCTCGCGCGCATCTGTGAC 2000
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 RESULT 13
 US-09-935-541-12
 ; Sequence 12, Application US/09935541
 ; Patent No. US20020150911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dietrich, Paul S.
 ; APPLICANT: McGivern, Joseph G.
 ; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
 ; TITLE OF INVENTION: AND USES
 ; FILE REFERENCE: R0043B-REG sequence listing
 ; CURRENT APPLICATION NUMBER: US/09/935,541
 ; CURRENT FILING DATE: 2001-08-23
 ; PRIOR APPLICATION NUMBER: 09/404,650
 ; PRIOR FILING DATE: 1999-09-23
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 6503
 ; TYPE: DNA
 ; ORGANISM: Rattus sp.
 US-09-935-541-12
 Alignment Scores:
 Pred. No.: 0 Length: 6503
 Score: 5407.00 Matches: 1234
 Percent Similarity: 61.05% Conservative: 241
 Best Local Similarity: 51.08% Mismatches: 502
 Query Match: 44.95% Indels: 444
 DB: 9 Gaps: 60
 US-09-611-257A-24 (1-2287) x US-09-935-541-12 (1-6503)
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 Qy 39 Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla----- 51
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 Qy 52 -----SerArgSerSerThrTh 57
 Db 234 TCCATGCCAAGGGTCTCTGCTCCACGCTGCATGGCTGACGCAACTTACCGCTCAT 293
 Qy 57 rCysProGlyProGly-----AlaAlaGlyAla-GlySerThr 70

Db 294 CTGAGCAGCCCGCGCCCTGAGCGCGGAATCACTGAGCAGCGCGGGCGCGGAGTCCCC 353
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 Db 354 CTCATCCCTCCAGCGCTGGAGGAGCCATTGGAAGGAACCAACCTGACGTCCACATC 413
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 Qy 166 alLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 186
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Qy	418	ettleAsnLeuCysLeuValVallleAlaThrGlnPheSerGluThrLysGlnArgGluS	438
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Db	1542	ACGCTGAGCCCGGTGATTGCTATGAGGAGATCTTCCAATATGTGTGCATCTCTCGCA	1601
Qy	478	ysAlaAlaArgArgLeuAlaGlnValSerArgAlalleGlyValArgAlaClyLeuLeus	498
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Db	1809	GCTGCCCTCACTGCCAGCACGAGCAGCGCGCCCTCTGGGCTGGGCGACACTGACT	1868
Qy	712	erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA	732
Db	1869	CAGCCCAAGAGCTCAGTTCTCGTGGCTCTGCAGAGCGCCGAGCAACATGGGGATGGAC	1928
Qy	732	laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu	749
Db	1929	TCCAGACGAGTGAAGTGGGTCTCTCGGACCTGGGGAAGGAGGAGGAACAGGAGGACG	1988
Qy	750	GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe	769
Db	1989	GGG-----CAGCCCGACTGTGTGGG-CATGTGTGGCGCGAGACACGAAAAAGCTG	2038

QY	770	ArgIysIleValAspSerLysTyrPheGlyIleMetIleAlaIleLeuValAsn	789
DB	2039	CGGGGCATCGTGGACAGCAAGTACTTCAACAGAGGTATCATGATGGCTACTCTGGTGAAC	2098
QY	790	ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu	809
DB	2099	ACATGCAGTCGGGCATCGAGCACCGAACAGCCGAGGAGCTGACCAACATCCTGGAG	2158
QY	810	IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal	829
DB	2159	ATTCGCAATGGGCTTCACCAAGTATGTTGCCCTGGAGATGATCCTGAAATGGCCGCC	2218
QY	830	TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal	849
DB	2219	TTTGGGCTCTTCGACTACCTCGGAAACCTTTACAACATCTTTGACAGCATCATCGTCAT	2278
QY	850	IleSerValTrpGluIleValGlnGlnGlyGlyLeuSerValLeuArgThrPhe	869
DB	2279	ATCAGCATCTGGAAATCTGGTGGCGACGGCGACGGTGCTGCTGCTGCGCACCTTC	2338
QY	870	ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal	889
DB	2339	CGGTTGCTCGGGTGCTGAAGCTGGTGGCTTCATGCGCGCTGCGGCGCCAGCTCGTG	2398
QY	890	ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle	909
DB	2399	GTGCTCATAGACCATCGAACACGTCGGCACCTTCTGCATGCTACTCATCTGCTTCATC	2458
QY	910	PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp	929
DB	2459	TTCATCTTCAGCATCTTGGGATGCAATCTTTGGCTGCAAAATTCAGCCTCCGCGACCGAC	2518
QY	930	---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr	948
DB	2519	ACGGAGACACCGTCTCTGCAGGAGAACTTCGATTCCTTACTGTGGGCCATCGTCACA	2578
QY	949	ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer	968
DB	2579	GTGTTCCAGATCCTCACTCAGGAGGACTGGAACGTTGCTCTGTACAAATGGCATGGCCCTC	2638
QY	969	ThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu	988
DB	2639	ACCACCCCTGGGCTCCCTCTATTTTGGTGGCCCTCATGACCTTGGCAACTACGTTCTC	2698
QY	989	PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys	1008
DB	2699	TTCAATCTCTGGTGGCTATCCTGGTAGAGGTTTCAGGCTGAGGGTGATGCTAATCGT	2758
QY	1009	SerGluSerGluProAspPhePheSerProSerValAspGly	1022
DB	2759	TCCTGCTCTGATGAGGACGAGAGCTCATCCAATTTGGAGGAGTTTGACAAGCTCCACAG	2818
QY	1023	-----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu	1040
DB	2819	GGCTGACCAACAGTAGAGATCTCAAGCTTGCCCAATACCCATGACACCAATGGACAC	2878
QY	1041	LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet	1058
DB	2879	CTGACCCCTAGCCTC-----CCTCTGGGTGGCATCTGGGCTCTGTGTGTTACCATGGGT	2932
QY	1059	SerHisProLysSerSerSerThrGlyValGlyValAlaLeuGlySerGlySerArgArg	1078
DB	2933	ACTGCCCGCGCTCTCACTGACGCCAGACCCGGTACTGTGGGCCCTTAGACTCTCGGAAA	2992
QY	1079	ThrSerSerSerGlySerAlaGluProGlyValAlaHisHisGluMetLysCysProPro	1098
DB	2993	AGCAGTGTCAATGCCCTG-----GGCAGATGAGCTATGATCAGCCATCCTTGTCCTC	3043
QY	1099	SerAlaArgSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg	1118
DB	3044	AGCTCCCGAGCTCTTACTACGGGCCCTGGGGCGGAGTGGGACCTGGGTAGTACCGCCCGC	3103
QY	1119	SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu	1138

Db 3104 TCAGCTGAAC-----AGCTGAACACAAAGCCGCTCAGCTGAG 3145
QY 1139 ArgSerLeuSerGlyGluGlnGluSer-----GlnAspGluGluSer 1156
Db 3146 CATGATCTCTACTGTCTGGGAGGTGAGGTAGCTGCTCAGGGCCTGTGAAGCGCC 3205
QY 1157 SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3206 CGGGAGGAGCGCCAACTCGCACCGCACCCCTGTCATGCTCCACACGCGCACGCGCAC 3265
QY 1170 -----ArgHisArgGlySerLeuArgGluAla 1179
Db 3266 CATGGACCCCACTGGCACACCGCTCACCGACACACCGCGGACTCTGCTCCCTGTATACC 3325
QY 1180 LysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer 1199
Db 3326 AGGGACTCTGTTACCTGGAGAGCTGTGTCGCGTGGTGGTGCCCACTCACGGGCGGCT 3385
QY 1200 -----GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly 1217
Db 3386 TGGAGGGGGCGGGTCAAGCCCTGGGCGAGGACTGCAATGGCAGATGCCCAAC----- 3442
QY 1218 ArgLeuAlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsn 1236
Db 3443 ---ATAGCCACGAGATGCTTCCACAGATGGATGACCGCGCGACCGCGGGGAGCGAG 3499
QY 1237 AspGluGlyAsnLeuSerLysGlyGluArgGlnGlnAlaTrpValArgSerArgLeuPro 1256
Db 3500 GAGGAGATCGACTATACCTGTGTTCCGGTCCGCAAGATGATGATGTGTACAGCGC 3559
QY 1257 AlaCysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPhe 1276
Db 3560 GACTGTGGGAAGTCGCGAGGACTGTCGCTACTCTCTTCCCGCCGAGAACAGATTC 3619
QY 1277 ArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIle 1296
Db 3620 CGGATCTGTGTACAGACCATCTGTCTCACAGCTTTTGTACCTGCTGTGGCCTTT 3679
QY 1297 IlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAla 1316
Db 3680 ATCTTCTCAACTGTATCACTTGTCTGGAGAGACCCGCAAGTTCGATGTGTAGCACT 3739
QY 1317 GluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMet 1336
Db 3740 GAGCGCATCTTCTCAGGTGTCTAATACATCTTCCAGGCCATCTTCTGCGGCGAGATG 3799
QY 1337 ThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSer 1356
Db 3800 ACATGAAGTGGTTTCTTGGGCTGTACTTTGGTGAGCAGCGGTACCTGGGTAGCAGC 3859
QY 1357 TrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet 1376
Db 3860 TGAATGTACTGGATGTTTCTCTGGTCTTTGGTGTCCATCATCATGATGCTGCTGCTACC 3919
QY 1377 ValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThr 1396
Db 3920 GCCTCTGTGGGGAGCCAGATCTGGGGGTCTTCCGGGTCTCGGGTCTCTGCTGCTACC 3979
QY 1397 LeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeu 1416
Db 3980 TTAGCTCTTTGAGGTATATCAGCGGGCCCTGGGCTGAAGCTGGTGTGTAGACGCTC 4039
QY 1417 MetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIle 1436
Db 4040 ATCTCTCCCTCAAGCCCATTTGGAAACATGCTGCTCATCTGCTGCTGCTCTTTCATCATC 4099
QY 1437 PheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheValCysGlnGlyGluAsp 1456
Db 4100 TTCGGCATCTGGGGGTGACGCTTTTCAAAGGCAAGTTCTACCATTTGTTGGAGTGGAC 4159
QY 1457 ThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHis 1476

Db 4160 ACCCGAAACATCACCAACCGGATCTGACTGCGTGGCGGCCAACTACCGTGGGTGCATCAC 4219
QY 1477 LysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLys 1496
Db 4220 AAATACAACTTTGACCAACTGGCCAGGCATTTGATGTCCTCTTTGCTCTTGGCTCCCAAG 4279
QY 1497 AspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPro 1516
Db 4280 GACGGCTGGTGAACATCATGTATATGATGATGATGCTGTGCTGTGGCAGCAGCCA 4339
QY 1517 IleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAla 1536
Db 4340 GTGACGAACCAACACCCCTGGATGCTACTGTACTTCAITTCCTTCTCTCATCTGTCAGC 4399
QY 1537 PhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGln 1556
Db 4400 TTCTTTGTGCTCAACATGTTGTGGCGGTGTCGTCGAGGAACTTCCACAAGTGGCGGCAG 4459
QY 1557 HisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLys 1576
Db 4460 CACAGAGGCTGAGAGCGCGGAGGCTGAGGAGAAACGGCTGGCGGCTTGGAAAG 4519
QY 1577 LysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAsp 1596
Db 4520 AAGCGCGT-----AAGGCTCAGAGGCTGCGCTACTATGCTACC 4558
QY 1597 TyrSerArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPhe 1616
Db 4559 TACTGTCCACAAAGCTGCTCATCTCCATGTCACCGACGACCTACTCTGGACATCTTC 4618
QY 1617 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1636
Db 4619 ATTACTTTCATCATCTGCTCAATGTTGTACCATGTCCTCGAGCAGCTACAACGAGCCT 4678
QY 1637 GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe 1656
Db 4679 ACATCCCTAGACAGACGCTTAAGTACTGCACTACATGTTCCACCTGCTTTGTGTGTG 4738
QY 1657 GluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsn 1676
Db 4739 GAGGTGTGCTGAAGCTGTGTGCAATTTGGCTGAGCGCTTTCTTCAAGACCGATGGAAC 4798
QY 1677 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGlu 1696
Db 4799 CAGCTGGACCTGCGCATCTGTGCTGTCGTCATGGGCATCACACTGAGGAGATCGAG 4858
QY 1697 ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1716
Db 4859 ATCAATGCGCGCTTCCCATCAACCCCACTCATCCGTCATGCTGCTTCTGCGTATC 4918
QY 1717 AlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal 1736
Db 4919 GCCCGGTGTGAAGCTATTGAAGATGGCCACAGGATGCGGGCCCTGCTGGACACAGTG 4978
QY 1737 MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle 1756
Db 4979 GTACAGGCTCTGCCCGAGTGGCAACCTGGCGCTCTCTTCATGCTGCTCTTCTTCATC 5038
QY 1757 PheAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys 1776
Db 5039 TATGCTGCTCTGGGAGTGGAGCTCTTCGGAAGCTGCTGCAATGAGGAGACCCGCTGT 5098
QY 1777 GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe 1796
Db 5099 GAGGGCATGAGCGGCGCACCGCCACTTTGAAACTTGGCATGCGCTTCTCAGCTCTTC 5158
QY 1797 ArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--- 1815
Db 5159 CAGGTCTCCACAGCGCATAACTGGAATGGAATATATGAGGACACCCCTGGCAGACTGACC 5218
QY 1816 AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer 1833
Db 5219 CATGATGAGCGCAGCTGCTTAAGCAGCTGCGAGTTGTGTGTCACCGCTCTACTTTGTGAGC 5278

Db	234	TCCATGCCAAGGCTCCCTGCTCCACGCTGCATGCTGACAGCAACTTACCGCCCTCAT	293	1305	TGATTTTCCAGGTGATCACTCTGGAAGGCTGGTGGAGATCATGTACTATGTGATGACG	1364	
Qy	57	rCysProGlyProGly-----AlaAlaGlyAla-GlySerThrG	70	Qy	398	laHisSerPheTyraSnPheIleTyraPheIleLeuLeuIleValGlySerPhePheM	418
Db	294	CTGCAGACGCCCGCCCTGAGCGGGGAATCACTGAGCAGCGGGGCCCGGAGTCCCG	353	Db	1365	CACATTTCTTACAACTTCACTTCTCTCTCATCATAGTGGCTCCTTCTTCA	1424
Qy	70	luLysAspProGlySerAlaAspSerGluAlaGluGly-----LeuProTyraP	86	Qy	418	etIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu	438
Db	354	CTTCATCCCTCCAGGCTGGAGGACCAATTGGAAGAAACCAACCTGAGCTCCCAATC	413	Db	1425	TGATCAACTTGTGCTCGTGTGTATAGCAACCCAGTCTCTGAGACCAAGCAACGGAGC	1484
Qy	86	roAlaLeuAlaProValValPhePheTyraLeuSerGlnAspSerArgProArgSerT	106	Qy	438	erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP	458
Db	414	CAGACCTGCTCTGTGCTTCTTCTGCTGCGCCAGACCCAGCGCCCAAGTGT	473	Db	1485	ACCGGCTGATGCTGAGCAACCGCCAGCGCTACTCTGCC---TCCAGCAGCGTGGCAGT	1541
Qy	106	ysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu	126	Qy	458	heSerGluProGlySerCysTyraGluGluLeuLeuLysTyraLeuValTyraIleLeuArgL	478
Db	474	GCATCAAGATGTTTGTAAACCGTGTGAGTGTGAGCATGTCTGTTATCTGCTGA	533	Db	1542	AGCGTGGAGCGCGGTGATGCTATGAGGAGATCTTCCAATATGTCTGCATCATCTTCGCA	1601
Qy	126	snCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	146	Qy	478	yeAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	498
Db	534	ACTGTGTACCTTGGCATGTACCAACCATGTGATGACATGAGTGCCTGTGACCGTT	593	Db	1602	AGCCCAAGCGC-----CGTGCCTAGGCTCTACCGAGCCCTG---1639	1639
Qy	146	ysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValAluMetValV	166	Qy	498	erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH	518
Db	594	GCAAGATCTCGAGGCTTTCGATGACTTTCATCTTCTTCTTCCATGAGTGTGTC	653	Db	1640	-----CAGA1643	1643
Qy	166	alLysMetValAlaLeuGlyIlePheGlyLysCysTyraLeuGlyAspThrTrpAsnA	186	Qy	518	isArgArgLeuSerValHisLeuValHisHisHisHisHisHisHisHisTyH	538
Db	654	TTAAGATGTGTGCTGGGCATTTTGGCAAGAGTGTACTCTCGGAGACACATGGAAC	713	Db	1644	ACCGCGCCGAGGCC-----1657	1657
Qy	186	rgLeuAspPheIleValIleAlaGlyMetLeuGluTyraSerLeuAspLeuGlnAsnV	206	Qy	538	isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA	558
Db	714	GCTGTGATTTCTCATGTATGTCAGCGAGGATGGTGTGAGTACTCTCTGGACCTACAGA	773	Db	1658	--ATGGCGCCGGGACA-----1672	1672
Qy	206	alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV	226	Qy	558	laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP	578
Db	774	TCAACCTGTCCAGCATCCGCTGCTGCTGAGGCTCTCAAGAGCCATCAACCGTG	833	Db	1673	-----CCAGCCCTGCCAAGCCTGGGCC-----1696	1696
Qy	246	alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnV	266	Qy	578	roProArgGlyAlaGluSerValHisSerPheTyraHisAlaAspCysHisLeuGluProV	598
Db	834	TACCCAGCATGGGATCTGGTGAACCTGCTGTCGACACGCTGCCCATCTGCGGGAAC	893	Db	1697	-----CATGCCAAG-----GAGCCCA1712	1712
Qy	266	alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA	266	Qy	598	alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlyS	618
Db	894	TGCTCTGCTCTGTTTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG	953	Db	1713	GCCACTGCAAGCTGTCACGACGACGACGACGACGACGACGACGACGACGACGACGAC	1750
Qy	286	laGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValA	286	Qy	618	erGlyLysValTyraProThrValHisThrSerProProProGluLeuLeuLysAspLysA	638
Db	954	CAGGCTGTCTAGGAACCGCTGCTTCTGGAAGAGAACTTCAACATACAGGGGATGTGG	1013	Db	1751	-----CCCACTCCCAACACA-----1765	1765
Qy	306	spleuGluProTyraTyraGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP	306	Qy	638	laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProP	658
Db	1014	CCCTGCCCTTATTATCAACACAGAGGAGATGACAGATGCCCTTATCTGCTCCCTGA	1073	Db	1766	--CTGTGCGAG-----1774	1774
Qy	326	roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGlyG	326	Qy	658	roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS	678
Db	1074	CTGGGACATGTCATCATGCTGCTGCGACGAGATCCCTCCATGAGGAGCAG-----	1126	Db	1775	-----CCCATCTCTGCCATCTCTG-----1792	1792
Qy	340	lyGlyProProCysSerLeu-----AspTyraGluThrTyraAsnSerS	340	Qy	678	erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspS	698
Db	1127	--GGCGGGAATGCTGCTGCTCCAAAGATGATGTGTATGACTTGGCGGGCGGCCAGG	1184	Db	1793	-----GCCCTGACCCACGCA1808	1808
Qy	358	erSerAsnThrThr-----CysValAsnTrpAsnGlnTyraTyraAsnCysSerAlaG	358	Qy	698	erCysProTyraCysAlaArg-----ThrGlyAlaGlyGluProGluS	712
Db	1185	ACCTCAACGCCAGCGGTCTGTGCTCACTGGAACCGCTACTACAACGCTGTGCGCAGCG	1244	Db	1809	GCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1868
Qy	378	lyGluHisAsnProPheLysGlyValIleAsnPheAspAsnIleGlyTyraAlaTrpIleA	378	Qy	712	erAlaAspHisValMetProAspSerAspSerGluAlaValTyraGluPheThrGlnAspA	732
Db	1245	GCNAACCCCAACCTCAACAGGGCGCCATCACTTTCACAACTTGTGCTATGCGGGATTG	1304	Db	1869	CAGGCGCAGGAAGGCTCAGGTTCTGTGTGCTCTGACAGGCGCCGAAGCAATGGGATGGAC	1928
Qy	398	laIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyraPheValMetAspA	398	Qy	732	laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu	749
			Db	1929	TCCAGACAGTGTGATGGGTCTCTCCGACCTCTGGGAGGAGGAGGAGGAGGAGGAGCAG	1988	

Qy	750	GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe	769
Db	1989	GGG-----CAGCCCGACTGTGTGGG-GATGTGTGGCGGAGACACGAAAAAGCTG	2038
Qy	770	ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn	789
Db	2039	CGGGGCATCTGGAGACAGCAAGTACTTCAACAGAGTATCATGATGGCTATCTCTGGTGAAC	2098
Qy	790	ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu	809
Db	2099	ACAGTCAGCATGGGCATCGACACCGAACAGCAGCCGAGGAGCTGACCAACATCTCGAG	2158
Qy	810	IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal	829
Db	2159	ATCTGCAATGTGGTCTTACCAGTATGTTTGTCCTCGAGATGATCTCTGAAACTGGCCGCC	2218
Qy	830	TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVal	849
Db	2219	TTTGGGCTCTTCGACTACCTGGGAACCCCTTACAAACATCTTTGACAGCATCATGTCAT	2278
Qy	850	IleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPhe	869
Db	2279	ATCAGCATCTGGGAAATCGTGGGCAGCGGACGGTGGCCCTGCTGCTGCGCACCTTC	2338
Qy	870	ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal	889
Db	2339	CGGTTGCTCGGGTGCTGAAGCTGGTGGCTTTCATGCCGGCGCTGCGCGCCAGCTCGTG	2398
Qy	890	ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle	909
Db	2399	GTGCTCATAGACACCATGGACAACGTGGCCACCTTCTGCAATGCTACTCATGCTGTTTCATC	2458
Qy	910	PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp	929
Db	2459	TTCAATCTTCAGCATCCTTGGATGCAATATCTTTGGCTGGCAAAATTCACCTCCGCAACG	2518
Qy	930	---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr	948
Db	2519	ACGGGAGACACCGTCTCTGACAGGAAGAACTTCGATTCTTCTACTGTGGGCCATCGTCACA	2578
Qy	949	ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer	968
Db	2579	GTGTTCAGATCTCTCACTCAGGAGGACTGGAAACGTTCTCTGTACAAATGATGCATGGCCTCC	2638
Qy	969	ThrSerSerTrpAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu	988
Db	2639	ACCACCCCTGGGCTCCCTCTATTTTGTGGCTCATGACCTTTGGCACTACGTTCTC	2698
Qy	989	PheAsnLeuLeuValAlaIleLeuValIleGlyPheGlnAlaGluGlyAspAlaThrLys	1008
Db	2699	TTCAATCTCTCTGGTGGCTATCTCTGTAGAGGGTTTCCAGGCTGAGGGTGATGCTAATCGT	2758
Qy	1009	SerGluSerGluProAspPhePheSerProSerValAspGly	1022
Db	2759	TCCTGCTCTGATGAGGACGAGCTCATCCAAATTTGGAGGAGTTTGACAAGCTCCACAG	2818
Qy	1023	-----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu	1040
Db	2819	GGCTGTGACCAACAGTAGAGATCTCAAGCTCTGCCAATACCCATGACACCCCAATGGACAC	2878
Qy	1041	LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet	1058
Db	2879	CTGACCCCTAGCCTC-----CCTCTGGGTGGCATCTGGGTCCTGTGGTACCATGGGT	2932
Qy	1059	SerHisProLysSerSerThrGlyValIleGlyAlaLeuGlySerGlySerArgArg	1078
Db	2933	ACTGCCCCCGCCCTCTCACTGCACCCAGACCCCGTACTGTGGTGGCCCTAGACTCTCGGAAA	2992
Qy	1079	ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProPro	1098
Db	2993	AGCAGTCTCATGTCCCTG-----GGCAGGATGAGCTATGATGACAGCATCCTTGTC	3043

Qy	1099	SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg	1111
Db	3044	AGCTCCGGAGCTCTACTACGGGGCCCTGGGGCGCAGCTGGGACTACGCCCGCC	3103
Qy	1119	SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu	1138
Db	3104	TCCAGCTGGAAC-----AGCTGAAACACAAGCGCCCTCAGCTGAG	3145
Qy	1139	ArgArgSerLeuLeuSerGlyGluGlyGlnGluSer-----GlnAspGluGluGluSer	1156
Db	3146	CATGAGTCCCTTACTGTCTGGGAGGTTGGAGGTAGCTGCCTCAGGCGCTGTGAAGCGCC	3205
Qy	1157	SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3206	CGGAGAGAGCGCCAACTCGCACCGCACCCCTGCATGCTCCACACCGCACCGACACGCGCAC	3265
Qy	1170	-----ArgHisArgGlySerLeuGluArgGluAla	1179
Db	3266	CATGGACCCCACTGGGCACACCTGCACCGACACCGCGGACTCTGCTCCCTTGATACC	3325
Qy	1180	LysSerSerPheAspLeuProAspTrpThrLeuGlnValProGlyLeuHisArgThrAlaSer	1199
Db	3326	AGGAGACTCTGTGACCTGGGAGAGCTGGTGCCTGGTGGTGGTCCCACTCACGGCGCGCT	3385
Qy	1200	-----GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly	1217
Db	3386	TGGAGGGGGCGGGCTCAGGCGCCCTGGGCGACAGGAGCTGCAATGGCAGATGCCCAAC	3442
Qy	1218	ArgLeuAlaArgThrLeuArgThrAsp--AspProGlnLeuAspGlyAspAspAspAsn	1236
Db	3443	---ATAGCCAAGGATGTTTCACCAAGATGATGACCGCGCGACCGCGGGAGGACGAG	3499
Qy	1237	AspGluGlyAsnLeuSerLysGlyGluArgGlnAlaTrpValArgSerArgLeuPro	1256
Db	3500	GAGAGATGACATATACCTCTGTTCCGGGTCCGCAAGATGATTGATGTGTACAGCCG	3559
Qy	1257	AlaCysCysArgGluArgAspSerTrpSerAlaTyrlPheProGlnSerArgPhe	1276
Db	3560	GACTGTGCGAAGTCCGCGAGGACTGTGTGCTACTCTCTCTCCCGCAGAACAAAGTTC	3619
Qy	1277	ArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIle	1296
Db	3620	CGGATCTGTGTGAGACCATCATGTGTCTCAAGCTTTTGTGACTACGTGGTCTTGGCCTTT	3679
Qy	1297	IlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAla	1316
Db	3680	ATCTTCTCAACTGTATCACCATTGTCTGGAGAGACCCAGATTGAAGCTGGTAGCACT	3739
Qy	1317	GluArgIlePheLeuThrLeuSerAsnTyrlIlePheThrAlaValPheLeuAlaGluMet	1336
Db	3740	GAGCGCATCTTCTCAGGGTGTCTAACTACATCTTCACAGCCATCTTCGTGGCGGAGATG	3799
Qy	1337	ThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlLeuArgSerSer	1356
Db	3800	ACACTGAAGTGTGTTCTCTGGGCCCTGTACTTTGGTGAGCAGCGTAGCTTGGCGTAGCAGC	3859
Qy	1357	TrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet	1376
Db	3860	TGGAAATGATCGATGTTTCTGGGTCTTTGTGTGTCATCATCATGATGCTAGTGTCCGGTG	3919
Qy	1377	ValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuArgThr	1396
Db	3920	GCCTCTGCTGGGGGAGCCAGATTCTGGGGGTCTCTCGGGTCTCTGCGCTCTCTGCTGCTACC	3979
Qy	1397	LeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeu	1416
Db	3980	TTACGTCTTTGAGGGTTATCAGCCGGGGCCCTTGGGCTGAAAGCTGTGTGTAGAGACGCTC	4039
Qy	1417	MetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIle	1436
Db	4040	ATTCCTCCCTCAAGGCCATTTGGGAACATGCTCTCATCTGTGTGCTCTCTTCATCATC	4099
Qy	1437	PheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAsp	1456

[illegible]

Search completed: April 28, 2005, 20:02:02
Job time : 2352 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 28, 2005, 07:20:16 ; Search time 9634 Seconds
(without alignments)

9036.017 Million cell updates/sec

Title: US-09-611-257A-24

Perfect score: 12028

Sequence: 1 MLPHRVPRCVTPPLRGSAR.....KKDTLSLGLSSDPTDMDPZ 2287

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -US09611257/runat_26042005_150449_14906/app_query.fasta_1.2439
-Q=/cgn2_1/USPTO_spool/US09611257/runat_26042005_150449_14906/app_query.fasta_1.2439
-DB=EST -QPMF=fastcap -SUFFIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257@cgn 1 1 6069 @runat_26042005_150449_14906 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1719.5	14.3	6636	3 BC043482	BC043482 Mus muscu
2	1698	14.1	6035	3 BC051413	BC051413 Mus muscu
3	1406	11.7	990	4 BT905383	BT905383 603167426
4	1385.5	11.5	939	4 BT736618	BT736618 603361089
5	1343	11.2	1076	4 BM479323	BM479323 AGENCOURT
6	1300	10.8	1064	4 BM451648	BM451648 AGENCOURT
7	1293.5	10.8	5666	9 AY416501	AY416501 Mus muscu
8	1275	10.6	879	7 CF548698	CF548698 AGENCOURT
9	1256.5	10.4	793	6 CA319705	CA319705 UI-M-FW0-

10	1230.5	10.2	5943	9	AY416499	Homo sapi
11	1198	10.0	715	7	CF745071	UI-M-GV0-
12	1197	10.0	810	5	BU709095	UI-M-EW0-
13	1195.5	9.9	952	7	CF584866	AGENCOURT
14	1190.5	9.9	4675	3	AK083220	Mus muscu
15	1187.5	9.9	771	5	BU058818	UI-M-FR0-
16	1185	9.9	736	4	BI160856	602864778
17	1182	9.8	711	5	BM950154	UI-M-EH0P
18	1172	9.7	777	5	BU708898	UI-M-FI0-
19	1163.5	9.7	957	4	EG298038	602396253
20	1162.5	9.7	777	6	CA945335	UI-M-FD0-
21	1141	9.5	973	2	BF783704	602109506
22	1140.5	9.5	828	2	BF606929	MY2 00012
23	1136.5	9.4	784	7	CF742232	UI-M-HB0-
24	1135	9.4	690	6	CB840838	M15E-1247
25	1112	9.2	6822	9	AY406058	Mus muscu
26	1111	9.2	6813	9	AY406056	Homo sapi
27	1103.5	9.2	845	6	CA327685	UI-M-FY0-
28	1102.5	9.2	773	4	BI249987	602995228
29	1096	9.1	676	4	BI917129	603181539
30	1088.5	9.0	727	5	BQ443110	UI-M-EV0-
31	1088	9.0	710	7	CR576255	CR576255
32	1079.5	9.0	647	6	CB518482	UI-M-GH0-
33	1075	8.9	667	7	CF531859	UI-M-GH0-
34	1074.5	8.9	731	7	CN534628	UI-M-HS0-
35	1067	8.9	707	7	CN216936	RJA002G02
36	1061.5	8.8	708	5	BQ179746	UI-M-EW0-
37	1059	8.8	693	5	BM949227	UI-M-EG0P
38	1055.5	8.8	803	6	CB245297	UI-M-FY0-
39	1034	8.6	843	5	BQ180375	UI-M-EX0-
40	1032.5	8.6	710	5	BU704267	UI-M-F00-
41	1018.5	8.5	684	5	BU262763	603374462
42	1012	8.4	772	6	CB524438	UI-M-FY0-
43	1011	8.4	652	2	BB660642	BB660642
44	1009	8.4	640	6	CB056097	NISC JJ12
45	997.5	8.3	658	5	BQ109588	imageqc_7

ALIGNMENTS

RESULT 1

BC043482

LOCUS

DEFINITION

BC043482

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

6636 bp mRNA linear HTC 19-NOV-2003
Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
mRNA (CDNA clone IMAGE:5369391), containing frame-shift errors.

BC043482.1 GI:28175783
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6636)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Casavant, T.L.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Db 1251 TGAGCTGCTGGGTGACTTTGTGAGCCTTGTGCATCTTTGGGCTCTTTGTGCTCAA 1310
Qy 420 nLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLe 440
Db 1311 CCTTGTGCTGGAGTCTTAAGCGGGAGTTCTCAAGGAAGAAAGAAAGGCAAGACAG 1370
Qy 440 uMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGl 460
Db 1371 AGTGACTTTTCAAGAGCTTCGG-----GA 1394
Qy 460 uProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAl 480
Db 1395 GAACAGCAGATGAAGAAGACCTTCGGGGCTACTCGGATCAGACACAGCGCTGAGGA 1454
Qy 480 aArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPr 500
Db 1455 GTTAGACTTTCATGACCCCTCA-----GTAGACGGCAACTTGGCTTCT----- 1497
Qy 500 oValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgAr 520
Db 1498 -CTTGCTGAAGAGGACGG-----CGGGGCCCATCGTAG 1529
Qy 520 gLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHis 540
Db 1530 G-----CAACTCAA 1538
Qy 540 yAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGl 560
Db 1539 TTCTGGCCCGCTTC-ATTCT-----AGCCCTGATGTG----- 1571
Qy 560 ySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPro-- 579
Db 1572 ----ATTGCCCTCTGAAACCCAGCACCAAGCCTGCAGCCACCCTA-GGCTTGGCCCAA 1626
Qy 580 -----ArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPr 597
Db 1627 TCTGGATCAGGGCAGAGAATCTCAACCCAGATTTCAGATCAACAAGACTC-CAACTAGTTCC 1685
Qy 597 oValArgCysGlnAlaProProArgCysProSerGluAlaSerGlyArgThrValGl 617
Db 1686 T-----TGTCCTTTAGATTGTGACC----- 1704
Qy 617 ySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLy 637
Db 1705 -----CTAATTCTGCCACCAAGCCACTCTCTCAG----- 1734
Qy 637 sAlaLeuValGluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIlePr 657
Db 1735 -----TTACAACATATCCCCACA--GGGCCAACAACTGTCTAGAGCTGACCAATAGGAG 1784
Qy 657 oProGlyPro-----PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGl 674
Db 1785 GCGCGGAGCGGTGGATGTTTCAG-----CACTACTCGCTCCACACTCCACCAG 1838
Qy 674 yAlaCysHisSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCy 694
Db 1839 CAGC---CAGCCAGCTCCAGCCAGTGTACACTGGCTCCATGACAGACACC----- 1887
Qy 694 sGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAs 714
Db 1888 -----CCTGGAGATCAGGATGAAGAAGA-GGGGA 1915
Qy 714 pHis-----ValMetProAspSerAspSerGluAlaValTyrGluPheThrGl 730
Db 1916 CCATGGCTAGTGTACAGCTGCT-----AAACA 1945
Qy 730 nAspAlaGlnHisSerAspLeuArgAspPro-HisSerArgArgGlnArgSerLeuG 750
Db 1946 AGATTATGAAACAAGATCTG-----CGCCACTTCCGCCGAGCCAAACGGGGTCTC- 1998
Qy 750 lyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheA 770
Db 1999 -----CGTGACCGTGC-----C 2011

Qy 770 rGlyIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnT 790
Db 2012 GCGGGCGCTCAAGTCAACGCCCTGCTACTGGGCTGTACTGCTGCTGCTCTCAACA 2071
Qy 790 hrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluI 810
Db 2072 CGTTGACCATAGCTTACAGACGACCATGGGAGCCCTTTGTGGCTCACCAGACCCCAAGAGT 2131
Qy 810 leSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLeuValT 830
Db 2132 ATGCCAACAAAGTTCTGCTCTGCTCTTCACTGTGGAGATGCTCCTCAAACTGTACGGCC 2191
Qy 830 yrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAsp-----G 845
Db 2192 TGGGCCCTCTGTCTAGTTGCCCTCTTTTCAACCGCTTTGACTGCTTGGTGTCTGTG 2251
Qy 845 lyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerV 865
Db 2252 GGGGCATCTTAGAAACCACTTTGTGTGGAGGTGGGGGCCATGCAGCCTCTTGGCATCTCAG 2311
Qy 865 alLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuG 885
Db 2312 TGCTCCGATGTGACGCTCTCTCAGGATCTTCAAGGTCAACAGGCACCTGGGCATCCCTGA 2371
Qy 885 lnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuL 905
Db 2372 GCATCTGGTGGCATCTTTGCTCAATTCATGAAGTCCATCGCTCTCTGCTGCTTCTCC 2431
Qy 905 euMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheA 925
Db 2432 TCTTCTCTTTCATCATCTCTCTCCCTGTGTCATGCAGCTGTTTGGGGCAAGTTCA 2491
Qy 925 laSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpA 945
Db 2492 ACTTTGACCAG-----ACCCACACCAAGAGGAGCACCTTTGTATACCTTCCCCCAAG 2542
Qy 945 laIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnG 965
Db 2543 CCTCTCTCACTGCTTCTCAGATCTGACTGTGTGAGGATTTGGACGTTGTATGATGATG 2602
Qy 965 lyMetAlaSer-----ThrSerSerTrpAlaAlaLeuTyrPheIleA 979
Db 2603 GTATCATGGCTACGTGGGCCCTTCTTCCAGGATGTGGTGGTGTATTATTCATCA 2662
Qy 979 laLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG 999
Db 2663 TCCTCTTCACTGTGGCAACTACATCTGTGTAACGTTTCTTGTCCATTCGCGTGGATA 2722
Qy 999 lyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProS 1019
Db 2723 ACCTA---GCCAGCGGGATGACGACCTGCCAAA----- 2754
Qy 1019 erValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisA 1039
Db 2755 -----GACAAAGGCGAGAGAG----- 2772
Qy 1039 laGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrProMetS 1059
Db 2773 -----AGCAGTGAAGGAA 2785
Qy 1059 erHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT 1079
Db 2786 ACCCTCCAAAGGAGCAAAAGTATTGGT----- 2814
Qy 1079 hrSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProS 1099
Db 2815 -----CCTGGTGGAGAGATGAGGACGCAAG-----G 2842
Qy 1099 erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS 1119
Db 2843 GTCAAGAAGATGAA-----CGTGACCGTGC----- 2856

Db 4784 GAAATCGATGTGACCTGAGTCTGACTTTGGCCGAGGAGGAATTTACCTGT---GGT 4840
 Qy 1824 ThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuVal 1843
 Db 4841 AGCAGTTTGGCATCGTCTACTTTCATCAGCTTCTTTATGCTCTGCTCTCTGCTGATATA 4900
 Qy 1844 AsnValValIleAlaValLeuMet----- 1851
 Db 4901 AATCTCTTTGGCTGTAATCATGATAAATTTGATTACCTTAACACAGAGATTGGTCTATC 4960
 Qy 1852 -----LysHisLeuGluGluSerAsnLysGluAlaLysGluAlaGluLeuGlu 1868
 Db 4961 CTGGAGCCCAACCACTTGTGAATTC---AAGAGGATCTGGTCTGAATATGACCCCGGA 5017
 Qy 1869 AlaGluLeuGluLeuGlu-----MetLysThrLeuSerProGln 1881
 Db 5018 GCCAAGGCCGATCAAGCACTTGGATGTGTTGCCCTGCTGAGACGATCCAGCCCA 5077
 Qy 1882 -----ProHisSer----- 1884
 Db 5078 TTGGGATTGGAAAGCTATGCCACACCGAGTGGCTGCAAGAGACTCGTGGCAATGAAT 5137
 Qy 1885 ---ProLeuGlySerProPhe-----LeuTrpProGlyVal 1895
 Db 5138 GTGCCCTCAACTCAGA-TGGAACAGTCACATTCACACGCTACACTCTTGGCCCTGGTGGC 5196
 Qy 1896 GlucyValAenSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIle 1915
 Db 5197 GACATCCTGAGATCAAGACAGAGGACCTGGATCAAGCCCAACAGGAGCTTCGGAT 5256
 Qy 1916 GlyAlaIleSerGlyPheSerLeuGluHisProThrMetVal-----ProHisProGlu 1933
 Db 5257 GGTCAACAAAGATCTGAAGCGGATAAAGCAGAAATTTGGATGAGGTTCATCCCTCC 5316
 Qy 1934 -----GluValProValPro---Leu 1939
 Db 5317 TCCGATGAGGAGGAGTCACTGTGGGAAATTTCTATGCCACACTCTCTGATCCCAAGATTA 5376
 Qy 1940 GlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsn 1959
 Db 5377 TTCCGAAATTCGGAGAGGAAGAAAGGGGCTACTAGGAAGAGAGC---CCCAAC 5433
 Qy 1960 AspSerTyrMetCysArgAsnGlySerThrAlaGluArgSer----- 1973
 Db 5434 AAGCACATCTCTCCCTCCAGGCTGTGCTAAGAGAGCTGCAGGACTTGGGTCTCGAT 5493
 Qy 1974 -----LeuGlyHisArgGlyTrpGlyLeuProLysLeuAlaGln 1985
 Db 5494 CCGTCAAGCCCTCACTATGACACTGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5553
 Qy 1986 SerGly-----SerIleLeuSerValHisSerGln 1995
 Db 5554 GGAGGTGAGGAG 5613
 Qy 1996 ProAla-----AspThrSerCysIleLeuGlnLeuProLysAsp 2008
 Db 5614 CCAGCCCAATCTCGATGGAATCTAGGATTT-CGGTGTCTCTACTCTGTTAAGAGAGAAC 5672
 Qy 2009 ValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPro 2028
 Db 5673 TTCCAGATTCTCTCACTGCGCCGAGTGTATGATGGGC-----TGCGCTCCCA 5723
 Qy 2029 ProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThr 2048
 Db 5724 ACTCCAGC---ACCCAGTGTGATACAGGTGCTGCCAACCCACACA----- 5768
 Qy 2049 AspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGly 2068
 Db 5769 -----GGAGAAGCTCTCGGG 5783
 Qy 2069 ProSerCysProLeuThrArg-----SerSerSerPheTrpGlyGlySer 2083
 Db 5784 TTTTCATGTTCACTATCCCGAAGAGAGAGATTTACGTCAAGGGAAGTCAAGGGCAGG 5843

Qy 2084 SerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeu 2103
 Db 5844 ACAATCAGATGAGAACAGAGAGTCCCTGACTGGACTCTGCTGATGAGCAGG--- 5900
 Qy 2104 ProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSer 2123
 Db 5901 -----CCGGGAGTC-----CTTCGAACCCAGTC 5924
 Qy 2124 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGln 2143
 Db 5925 TTTTACCACTCACTGG-TCCCAGCAACACGTAACGGGACCATGTGCCACGCCGAGT 5983
 Qy 2144 GluGluProLeuPheProArgAspLeuLysCysTyrSerValGluThrGlnSerCys 2163
 Db 5984 TTGCTGCCCCCAGCCCTCGAGGTCGGAAGCCCTCTTCCATCCAG-----TGT 6034
 Qy 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCys 2183
 Db 6035 CTGCAACGCCAGGCG-----AGTTGT 6055
 Qy 2184 LeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeu----- 2199
 Db 6056 GAGATTT---ACCTATCCAGCACCTACCTCGTGGACGACCTCAGGACCAAGCAG 6111
 Qy 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro--- 2218
 Db 6112 GGCTCAGGTTCTTGGGCGCCCTCTCTCAGAGGTCGACTGTATATGCCCCCTGTT 6171
 Qy 2218 ----- 2218
 Db 6172 GTTGGTGGAGAACTCTACAGTGGTGAAGGATACCTTGGCAAACTTGGCGGCCACTGCG 6231
 Qy 2219 -----SerIleSerIleAspProProGluSerGlnGlySerArgProPro--- 2233
 Db 6232 TACCTTCACCTGTCTGCAAGTGGCTGGAGTCTATCCGAATCCCAAGCCAGAGAGGG 6291
 Qy 2234 ---Cys-----SerProGlyValCysLeuArgArgAlaProAlaSerAspSerLys 2250
 Db 6292 CAGTGTCTGACAGTTTGGTGGAGGCTGTCTCATCTCCGAGGCTTAGTCTCTTTGCCCA 6351
 Qy 2251 AspProSerValSerSerPro-----LeuAspSerThrAlaAlaSerProSerPro 2267
 Db 6352 AGACCCACGATTTGTGGCCCTGTGCCAGGAGGATTCAGATGTCATGTACCTGACCT 6411

RESULT 2

BC051413

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC051413 6035 bp mRNA linear HTC 19-NOV-2003
 Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
 mRNA (CDNA clone IMAGE:6493332), containing frame-shift errors.
 BC051413
 BC051413.1 GI:30802106
 HTC.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 6035)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzyzanski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 6035)
Straussberg, R.
Direct Submission
Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapps-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsourgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 108 Row: 0 Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

FEATURES

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/clone="IMAGE:6493332"
/tissue_type="Eye, retina, mouse strain C57Bl/6"
/clone_lib="NIH_MGC_94"
/lab_hosts="DH10B"
/note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 3,53e-106 Length: 6035
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Percent Similarity: 38.96% Conservative: 338
Best Local Similarity: 25.14% Mismatches: 767
Query Match: 14.12% Indels: 730
DB: 3 Gaps: 83

US-09-611-257A-24 (1-2287) x BC051413 (1-6035)

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Qy 56 ThrThr-----CysProGlyPro----- 61
Dy 72 GGGACTGCGCCCTGGCCCTGAATGGGGCTGTCTCTGGGCTTCAACTGTGGGACTGAT 131
Qy 62 -----GlyAlaAlaGlyAlaGlySerThrGluGlyAspProGlySerAlaAlaSerGlu 79
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Db 132 ACCAGCGGGCGTCAGGCTGGGACCCCAAGAAAGAGAGCCAGCACACAAACACAAG 191
Qy 80 AlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAsp 99
Db 192 ACTGTGGCGGTGGCCAGTCGCTCAGAGATCACCTCGAGCGCTCTTCTGCCTCACCTTACT 251
Qy 100 SerArgProArgSerTrpCysLeuArgThrValCysAsnProTyr-----PheGlyArg 117
Dy 252 AATCCATTCTGGTCTGCTGCTGATCAGCATGTTGA-----GAGTGAAGCCCTTTGATATT 305
Qy 118 ValSerMetLeuValLeuLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlu 137
Db 306 CTCATCTCTCTGACATCTTTGGCAACTGCTGGCATTGGGGTATATATATATATATATAT 365
Qy 138 AspLeuAlaCysAspSerGlnArgCysArgLeuLeuGlnAlaPheAspPheLeuPhe 157
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Qy 158 ---AlaPhePheAlaValGluMetValValValMetValAlaLeuGly---IlePheGly 175
Db 420 CTGGTGTATTTTCCCTGGAGACAGTGTCAAGATCGTAGCTATGGGCTGGTCCAT 479
Qy 176 LysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValleAlaGly 195
Db 480 CCCAGCGCTATATTCGCAATGGCTGGAACCTGCTCGACTTCATCATCTGCTGCTGGG 539
Qy 196 MetLeuGlyTyrSerLeuAspLeu----- 203
Db 540 CTGTTTCAGCGTCTCTCTGGAACAAGAGCTGGCGCCGAGGAGATGCCCGCATACTGA 599
Qy 204 -----GlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 220
Db 600 GGAAGCCAGGAGGCTTCGATGTAAGGACACTGCGGGCTTTAGGGTGTCTACGACCTCTA 659
Qy 221 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeu 240
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Qy 241 ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIleGlyIleVal 260
Db 720 GTGCGCGCTCTGCACATTCCTCTGTGGTGTCTTCGTCATTCATTATACCCCATC 779
Qy 261 GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer 280
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Qy 281 LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro 300
Db 825 -----CTGGGATCTGATATGGAA-----GCAGAGGAGGAGCCCATCACCT 863
Qy 301 PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu 320
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Qy 321 ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer 340
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Qy 341 SerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis 360
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Qy	1852	-----LyHisIleuGluGluSerAsnLysGluAlaLysGluG	1864
Db	4344	GAGATTGGTCTATCTCGGACCCACCACCATCTTGTGAAATTC---AAGAGGATCTGGTCTG	4400
Qy	1864	luAlaGluLeuGluAlaGluLeuGlu-----MetLysT	1877
Db	4401	AATATGACCCCGGACCCAAAGCGGCATCAAGCACTTGGATGTGGTTGCCCTCTCTGAGAC	4460
Qy	1877	hrLeuSerProGln-----ProHisSer-----	1884
Db	4461	GCATCCAGCCCATTTGGGATTTGGAAAGCTATGCCCCACACCGAGTGGCCTGCAAGAGAC	4520
Qy	1885	-----ProLeuGlySerProPhe-----L	1891
Db	4521	TCGTGGCAATGAATGTCCTCCCTCAACTCAGA-TGGACAGTGACATTCACAGTCACTC	4579
Qy	1891	euTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyValAlaProHist	1911
Db	4580	TTTGCCCTGTGGGACATCCCTGAAGATCAAGACAGCAAGGAACCTTGGATCAAGCCAAC	4639
Qy	1911	hrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetVal----	1929
Db	4640	CAGGAGCTTCGGATGGTTCATCAAAAAGATCTGGAAGCGGATAAAGCAGAAATTTGTTGGAT	4699
Qy	1930	--ProHisProGlu-----GluValP	1936
Db	4700	GAGGTCACTCCCTCTCCCGATGAGGAGGAGGTCACTGTGGGAAAAATTTCTATGCCACATTC	4759
Qy	1936	roValPro---LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrH	1955
Db	4760	CTGATCCAGATTATTTCCGAAATTTCCGAGAGAAGAAAGGGGCTACTAGGAAGA	4819
Qy	1955	isSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSer----	1973
Db	4820	GAGGC---CCCAACAAGCACATCTCTGCTCCAGGCTGGTCTAAGGAGCCTGCAGGAC	4876
Qy	1974	-----LeuGlyHisArgGlyTyrPGLY	1981
Db	4877	TTGGGTCTTGAGATCCGTCAAGCCCTCACCTATGACACTGAGGAAGAAGGAGGAGGAA	4936
Qy	1981	euProLysAlaGlnSerGly-----SerIleLeuS	1991
Db	4937	GAGCAGTGGGTGAGGAGGTGAGGAAGAGAGAGCTGAGAACACCCAGAACCATCAAA	4996
Qy	1991	erValHisSerGlnProAla-----AspThrSerCysIleLeuG	2004
Db	4997	GACTCCATAGACTCCAGACCCCAATCTCGATGGAACTCTAGGATTT-CGGTGTCTCTACC	5055
Qy	2004	lnLeuProLysAspValHisTyrIleuLeuGlnProHisGlyAlaProThrTrpGlyAlaI	2024
Db	5056	TGTTAAGGAGAAATCTCCAGATTCTCTCAAATCTGGGCCGAGTGATGATGGGC----	5111
Qy	2024	leProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnA	2044
Db	5112	-----TGCTCCCAACTCCAGGC---AGCCCAAGTGTGATACAGCGTGGCTCCCAACCA	5163
Qy	2044	laAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuS	2064
Db	5164	CA-----G	5166
Qy	2064	erGluValSerGlyProSerCysProLeuThrArg-----SerSerSerP	2079
Db	5167	GAGAAGCTCTGGGGTTTTTCATGTGTTCACTATCCCGGAAGAAGGAATATTTCAGCTCAAGGG	5226
Qy	2079	heTrpGlyGlySerSerIleGlnValGlnArgSerGlyIleGlnSerLysValSerL	2099
Db	5227	AACTCAGGCGGACGACAAATCAGAATAGGAACAGGAAGTCCTGACTGGGACTCTGACCT	5286

Qy	2099	yshtslleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProp	2111
Db	5287	GGATGACGAGG-----CCGGGACTT	5307
Qy	2119	roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuL	2139
Db	5308	TTCGAACCCAGTCTTTTACCACCTACTGG-TCCGAGCAACAGTNAACGGCACCATG	5366
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Db	5447	-----AGTTGTGAAGATT-----ACCTATCCCAGGCACCTACCATCTGTGACGGACC	5494
Qy	2199	eu-----GlyGlyGlnProLeuGlyProGlySerArgProLysLysLysL	2215
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Qy	2215	euSerProPro-----	2218
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Qy	2219	-----SerIleSerIleAspProProGluSerGlnGlySerArgP	2232
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DEFINITION	mRNA sequence.		
ACCESSION	BI905383		
VERSION	BI905383.1	GI:16167886	
KEYWORDS	EST,		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 990)		
JOURNAL	NTH-MGC http://mgc.nci.nih.gov/		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-x@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11645 row: d column: 08 High quality sequence stop: 911. Location/Qualifiers		
FEATURES			

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/lab_host="NIH CGAP Lu33"
/notes="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5]. TGTACCAATCGAAGTGGAGCGCGCTCTGTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Alignment Scores:
Pred. No.: 3,84e-87 Length: 990
Score: 1406.00 Matches: 293
Percent Similarity: 90.77% Conservativeness: 2
Best Local Similarity: 90.15% Mismatches: 22
Query Match: 11.69% Indels: 9
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x BI905383 (1-990)

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QY 1842 uValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLys 1862
Db 61 GGTCAAGTGTCTATGCGCTGCTGATGAACACCTGGAGAGAGACCAACAGAGGCCAA 120
QY 1862 sGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnPr 1882
Db 121 GGAGGAGCGGAGTTGGAGCGGAGCTGGAGCTAGAGATGAACACACTCAGCCCGCAGCC 180
QY 1882 oHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAs 1902
Db 181 CCACCTCCCGCTGGCAGCGCCCTTCTCTGCTGGGTGGAGGTGTCAATAGCCCTGA 240
QY 1902 pSerProLysProGlyValAlaProHisThrThrAlaHisIleGlyAlaAla---SerGlyPh 1921
Db 241 CAGCCCTAAGCTTGGGGCTCCACACACCGCCGCCACATTTGGAGCAGCCTTTCAGGCTT 300
QY 1921 eSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyPr 1941
Db 301 CTCCTTGAGCACCACCCACGATGTACTCTACACTGAGAGGGGCCAGTCCCGCTAGGACC 360
QY 1941 oAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSe 1961
Db 361 AGACCTGCTCACTGTGAGGAAGTCTGGTGTGACCGGACACACTCTCTGCCCCAATGACAG 420
QY 1961 rTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLe 1981
Db 421 CTACATGTGCGGCAATGGGAGCACTGCCGAGAGATCCCTAGGACACAGGGGCTGGGGCT 480
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Db 481 CCCCCAAGCCAGTCAGGCTCCATCTTGTCTTCACTCCCAACCCAGCAGACACACGCTG 540
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QY 2021 pGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuAr 2041

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Db 601 GGGGCCATCCCTAAACTACCCACCTGGCGCTCCCTCTGGCTCAGAGGCTCTCAG 660
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QY 2061 pLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrp-G 2081
Db 721 CTGTTGTTCAGAGGTAGTGGCCCTCTGCTCTGACCCGTCC-TCATCTCTCTGGG 779
QY 2081 lYGlySerSerIleGlnValGlnGlnArgSer---GlyIleGlnSerLysValSerLys- 2099
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QY 2100 HisIleArgLeuPro-AlaProCysPro-GlyLeuGlu-ProSerTrpAlaLysAspPro 2118
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RESULT 4
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ACCESSION BI736618
VERSION BI736618.1 GI:15713631
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1936 row: b column: 23
High quality sequence stop: 853.
FEATURES
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores: 9,39e-86 Length: 939
Pred. No.: 1385.50 Matches: 282
Score: 92.48% Conservativeness: 1
Percent Similarity:

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Best Local Similarity: 92.16% Mismatches: 18
Query Match: 11.52% Indels: 8
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x BM479323 (1-939)

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Qy 1970 AlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIle 1989
Db 63 GCCGAGAGATCCCTAGGACACAGGGGCTGGGGGCTCCCAAGGCCAGTCAAGGTCCATC 122

Qy 1990 LeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspVal 2009
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Qy 2010 HisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProPro 2029
Db 183 CACTATCTGTCTCCAGCCTCATGGGCTCCCACTGGGGCGGCATCCCTAAACTACCCCA 242

Qy 2030 ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAsp 2049
Db 243 CCTGGCGGCTCCCTCTGGCTCAGAGGCTCTCAGGGCCAGGAGCAATTAAGACTGAC 302

Qy 2050 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPro 2069
Db 303 TCCCTGGACGTGCGAGGGCTGGGTAGCGGGAGACCTGTGTCTCAGAGTGAGTGGGCC 362

Qy 2070 SerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIleGlnValGlnGln 2089
Db 363 TCCTGCCCTCTGACCCGCTCTCATCTCTTCTGGGGCGGTGTCAGCATCCAGTGCAGCAG 422

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Qy 2110 LeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThr 2129
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Qy 2130 GluLeuSerTrpIleSerGlyAspLeuLeuProSerGlnGlnGluProLeuPhePro 2149
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Qy 2249 SerLysAspPro 2252
Db 894 TCGAAGGATCCT 905

RESULT 5
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LOCUS
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ACCESSION BM479323
VERSION BM479323.1 GI:18528365
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1076)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 692.
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Site2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1,06e-82 Length: 1076
Score: 1343.00 Matches: 281
Percent Similarity: 87.23% Conservative: 6
Best Local Similarity: 85.41% Mismatches: 19
Query Match: 11.17% Indels: 23
DB: 4 Gaps: 4

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Db 3 AGGACATCATCAATAAATCGGACTGTCCGAGGCCAGTACCGGTGGGTCCGACACAG 62

Qy 1478 TyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp 1497
Db 63 TACAACCTTGACAACCTTGCCAGGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122

Qy 1498 GlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIle 1517
Db 123 GGTGGGTGGACATCATGTAGATGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 182

Qy 1518 MetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhe 1537
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Qy 1538 PheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHis 1557
Db 243 TTTGTCTCTGAACATGTTTGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 302

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402 TCCCGCTTCGGCTCTCGTCCACCACTTGTGCACGACCACTACTCGGACCTCTTCATC 461
1618 ThrGlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnProGln 1637
462 ACAGGTGTTCATCGGGCTGAACGTGTGCACATGGCCATGGACACTTACACAGAGCCCGAG 521
1638 IleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGlu 1657
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582 TCAGTTTTCAAACTTGTGGCTTGTGTTCCGTCGGTCTTCCAGGACAGGTGGAAACAG 641
1678 LeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluVal 1697
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1698 AsnLeuSerLeuProIleAsnProThrIleIleArgIle-MetArgValLeuArgIleAl 1717
702 AACGCTCGTGGCCATCAACCCATCATCGCATCATTTGAGGTGCTGGCAATGCG 761
1717 ArgValLeuLysLeuLeu-LysMetAlaValGlyMet-ArgAlaLeuLeuHisThrVal 1736
762 CCGAGTCTGAAGCTGTGAAATATGCTGTGGCATGCGCGCGCTGTGGACACCGTG 821
1737 MetGlnAla--LeuProGlnValGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuP 1754
822 ATGACGCCCCCTGTCCCGGTGGGAAACCTGGGACTTTTCTCCAGGCCCTGTGGTTT 881
1754 hePheIlePheAlaAlaLeuGlyVal-----GluLeuPheGlyAspLeuGluCysAspG 1772
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1772 LuThrHisProCysGlu 1777
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ACCESSION BM451648
VERSION BM451648.1 GI:18500688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1064)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2116 row: h column: 02
High quality sequence stop: 657.
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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Best Local Similarity: 76.39% Mismatches: 20
Query Match: 10.81% Indels: 56
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QY 1515 GlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIle 1534
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Db 361 GCTTCCGGCAGCTCAGCCAGCGCTGGTCAGAAAGCCAGTGCAGAACCTTACTTCCGAC 420
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QY 1617 IleThrGlyValIleGlyLeuAsnValThrMetAlaMetGluHisTyrGlnGlnPro 1636
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Db 661 CAGCTGACCTGGNCACTTGTCTGCTCATCATGGCATCATCGCTGGAGAAATCGAG 720
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Db	Db	841	GATGCCAGGCCCTGCCAGGTGGGAAACCTGGGAACCTTCCCTCCAGGTGGTGT	900
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DEFINITION			Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	
ACCESSION		AY416501	GI:39772461	
VERSION			GSS.	
KEYWORDS				
SOURCE			Mus musculus (house mouse)	
ORGANISM			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE			1 (bases 1 to 5666)	
AUTHORS			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE			Infering nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL			Science 302 (5652), 1960-1963 (2003)	
PUBMED			14671302	
REFERENCE			2 (bases 1 to 5666)	
AUTHORS			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE			Direct Submission	
JOURNAL			Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
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Query Match:	10.75%	Indels:	755	
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952	Db	ATGCTAGAACCTTGTCTCTCGGGAACAGCTCTGACCGCGGCAATGCGCAGAGGGTTC	1707	Db	GAACGAGTTCGACAGCAGCAGCAGCAGTGGAGAAAGTGAGGGCCGCGCGCATC
350	Qy	GlnTyTyThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPhe	677	Qy	isSerSerCysLysIleSerSerProCysSer-----
1012	Db	-----TGATGAAGACAGGAAGAAATCCAACTACGGCTACACAGCTTC	1767	Db	GCTCTTATCCCGA---TCCGCGCCCGCAGCGCCGCGCAGCAGCTACAGCGG
370	Qy	AspAsnIleGlyTyxAlaTrpIleAlaIlePheGlnValIleThrLeuGluTyTrpVal	688	Qy	-----LysAlaAspSerGlyAlaCysGlyPro-----
1060	Db	GACACCTTCAGCTGGGCTCTCTGGCACTGTTCCGCTCATGCTCATGACAGCTACGGAG	1824	Db	CTACAGCCAGTGCAGCCGCTCGTCGCGCATCTTCCCGAGCTTCGCGCAGCGTGAACG
390	Qy	AspIleMetTyPheValMetAspAlaHisSerPheTyAsnPheIleTyPheIleLeu	697	Qy	-----AspSerCysProTyCysAlaArgThrGlyAlaGlyGluProGln
1120	Db	AACTTATACAGCTGACCTTACGAGCGGCTGGGAAACGTACATGATCTTCTTGTCTTG	1884	Db	CAACAGCACCTGGACTGCAATGCGGTGCTGCTCATCGGCTC-GGC-----TCGC
410	Qy	LeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGln	712	Qy	erAlaAspHisValMetProAspSerAspSerGluAlaValTyGluPheThrGlnAsp
1180	Db	GTGATCTTCTGGGCTTCTTATTGGAACCTTGTGCTGCTGGTGGCCATGGCT	1937	Db	ACATCGGGCGCTCTGCTGAGGCAACACTGAGGTGGAGATTAAAG-----
430	Qy	PheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeu	732	Qy	laGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProA
1240	Db	TACGAAGAG-----	1984	Db	-----A
450	Qy	SerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyTrpGluGluLeu	752	Qy	spAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLys
1249	Db	CAGAACAGGCAACACTGGAGGAGGAGCAGCAGAAAGAGCAGAGTCAAGGCGATGCTG	1985	Db	AGAAAGCCCTGGATCGCTCTTAGTCTCCATGGAACTCGCTCCTACGAGCGGAAG
470	Qy	LysTyTrpLeuValTyTrpIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAla	772	Qy	--IleValAspSerLysTyTrpPheGlyArgGlyIleMetIleAlaIleLeuValThrL
1309	Db	GAGCAGCTC-----AGAAGCAGCAGGAGGAGCGCAGTCAAGATGCC	2045	Db	ACAGATCAACAGT-----ATAATGAGCGTTGTCACAAACAC
490	Qy	IleGlyValArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGlu	791	Qy	eu-----
1354	Db	ATT-----GAAGAAAGGGGAGATGGGTA	2084	Db	TAGTGAAGNN
508	Qy	-----ProGlnProSerGly-SerCysThrArgSerHisArgLeuSerValHisH	791	Qy	-----
1381	Db	GGCTCTCGAGGAGCTCATCTGAGCTCTTAACTCA-----	2144	Db	NN
525	Qy	sLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis	791	Qy	-----
1417	Db	-----	2204	Db	NN
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1418	Db	-GTTCCAGAGCGGAGGAGCGTCCGNAACCGACCGGAAGAGAGAGAGAGAGAGCTC	2264	Db	NN
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1477	Db	TCTGAAG-----GGGAGGAGAGAGGGGAGC-----	2324	Db	NNNNNNNGTGTCTACTGGGATCTTCACGGCGGAAATGTCTCTGAAGCTCATAGCCATCG
585	Qy	lHisSerPheTyHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr	831	Qy	lyProPheGlyTyTrpIleLysAsnProTyTrpAsnIlePheAspGlyValIleValIleS
1502	Db	-----CCGAG	2384	Db	ATCCCTACTATTACTTCCAAGAGAGGCTGGAAACATTTTACGCGATTATTCGCTCCTCA
605	Qy	oArgCysProSerGluAla-----SerGly-----ArgTh	851	Qy	erValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgL
1507	Db	AAGTGTATTAGTCAGATCGGAGATGGCATGGAAGAGGCTTCGCGCTGCCAGAC	2444	Db	GTTTATGAGCTGGGCTTGCAGAGCTGGGCGCTCTCAGTGTCTGCTGCTTCCGAT
615	Qy	rValGlySerGlyLysValTyTrpThrValHisThrSerProProGluIleLeuLys	871	Qy	euMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValVal
1567	Db	AATAGGATA-GGGAGGAAATTTTC-----ATCAT	891	Qy	euMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheI
635	Qy	sAspLysAlaLeuValGluAlaProSerProGlyProProThrLeuThrSerPheAs	2564	Db	TTGGGAACCTCCGTGGCGCCCTGGGCAACCTGACCTGGTGTGGCCATCATTTGCTTCA
1596	Db	GAATCAGTGGCTGCTCAGCATC-----CCAGCTCGCCCTTCTTCCCGACACAA	911	Qy	lePheSerIleLeuGlyMetHisLeuPheGly-----CysLysP
655	Qy	nilePro-----ProGlyProPhe-----	2624	Db	TCITTGGCGGTGGGATGACGCTCTTTGGAAAGAGCTACAAGGAGTGGCTGTCTGAAGA

Qy	924	heAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPhaAspSerLeuLeuT	944
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Db	2732	ACTCCTTCCTCATCGTCTTCGAGTGTGTGGGGAGTGTATCGACGACGAGTGTCTGAAC	2791
Qy	962	eutYrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT	982
Db	2792	TTATTTCTGGCCTTGCTTCTGAG-----	2814
Qy	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	2815	-----CTCCTTCAAGCAGACAAT	2833
Qy	1002	laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG	1022
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Qy	1022	lyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA	1042
Db	2882	GTGATCCGATCAAGAAGGGCGT-----GGCCTGGGCCAA-----	2916
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Db	2917	-----AGTCAAGGTG	2926
Qy	1062	ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers	1082
Db	2927	CATGCCTTCATGACGCACACTTCAACCAACGGGAGCGCTCATGAGTGAACCTTTAGAC	2986
Qy	1082	erGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProProSerAlaArgS	1102
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Qy	1102	erSerProHisSerProTIpSerAlaAlaSerSerTIpThrSerArgArgSerSerArgA	1122
Db	3022	-----CCACACCG-----GCCTGGACATTCACGAAGTCGGGACTTCAGAAAAAATGGAAATGG	3075
Qy	1122	snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL	1142
Db	3076	CACCACCTAGCGCATCGGCCAAAACGTG-----	3101
Qy	1142	euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgA	1162
Db	3102	-----GACGATACCGTCTCTCAGAA-----	3122
Qy	1162	laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers	1182
Db	3123	-----GGGAGTA	3129
Qy	1182	erPheAspLeu-----ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyA	1201
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Db	3220	TCCAGAGGTTCAAG-----TGCTGCCAGG	3243
Qy	1261	luArg-----AspSerTrpSerAlaTyIlePheProProGlnSerA	1275
Db	3244	TCAACATCGAGGAAGGACTAGGCAAGTCGTGG-----TGATC-----	3281

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Db	3460	AGATGTTGCTCAAATGGACAGCATGCGCTTCGTC-----AAGTCTTCACCA	3507
Qy	1355	erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValS	1375
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Qy	1395	rgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluT	1415
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Qy	1469	-----AlaSerTyrArgTrpValArgHisIysTyrAsnPheAspAsnL	1483
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Qy	1543	heValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluA	1563
Db	4099	TCATCGGTGCATCATCGACATTTCAATCAACAGAGAAAAGATTGGAGGTCAGGACA	4158
Qy	1563	la---ArgArgArgGluGlyArgLeuArgArgLeuGluLysLysArgArgSerLysG	1582
Db	4159	TCITCATGACAGAGGAACAGAAGTACTACAACGCCATGAAGAAGCTAGGCTCCAAGA	4218
Qy	1582	luLysGlnMetAlaGluAlaGlnCysIleAspProTyrTyrSerAspTyrSerArgPheArgL	1602
Db	4219	AGCCACAG-----AAGCCCATCCCGCACCTTTTGAAACAAATCCAAG	4260
Qy	1602	euleuValHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleG	1622
Db	4261	GGATTTGCTTTGATTCGTCCGCAACAAGCCCTTCGACATCTCGTATGATGATGCTCATCT	4320
Qy	1622	lyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluA	1642


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Db 4321 GCCTTAACATGGTGACCATCATGGTGGAGACACACACAGACAGCAGTGGGAGACA 4380
Qy 1642 laLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysL 1662
Db 4381 TTCTCTACTGGATTAATCTGGTCTTCTGTCATCTTCTTCACTCGAGTGTGTCTCAAAA 4440
Qy 1662 euValAlaPheAlaPheArgArg---PhePheGlnAspArgTTPAsnGlnLeuAspLeuA 1681
Db 4441 TG-----TTTGGCTTGAGACACTACTATTTCACCATGGCTGGAACATCTTTGACTTGG 4494
Qy 1681 laIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerL 1701
Db 4495 TGGTGGTCATCTCTCAATTTGGGAATGTCTTGGCTGATATCATTTGAGAAGTACTTC- 4553
Qy 1701 euProfileAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuL 1721
Db 4554 -----GFTCTCCCGACCCATTCTCGGCTCATCGGATGGCCGCGCATCGGCGCATCTTGC 4608
Qy 1721 ysLeuLeuLysMetAlaValGlyMetArgAlaIleLeuHisThrValMetGlnAlaLeuP 1741
Db 4609 GTCTGATCAAGGGCGCCAAAGGATCCGCACCCCTGTCTTTGGCTTAATGATGTGCGTGC 4668
Qy 1741 roGlnValGlyAsnLeuGlyLeuPheMetLeuLeuPheIlePheAlaAlaLeuG 1761
Db 4669 CCGCCCTGTTCACATCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4728
Qy 1761 lyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyA 1781
Db 4729 GGATGTCCAATTCGCGTCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 4773
Qy 1781 rghIsAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrG 1801
Db 4774 ACATGTTCACTTCGACAGCTTTGGCAACAGCATGATCTCCCTGTTCCAGATCAGCACCT 4833
Qy 1801 lyAspAsnTrpAsnGlyIleMet-----LysAspProSerArgAspCysA 1816
Db 4834 CTGCTGGTGGGATGGCTTACTGTGCTCAATCTCGAACCCGCCCTGACTGCGAGCTGG 4893
Qy 1816 spGlnGlu-----SerThrCysTyrAsnThrValIleSerProI 1829
Db 4894 ACAAGGAGCACCCAGGAAGTGGCTTCAAGGGGAGCTCGGGGAACCCCTCGTGGGCACT 4953
Qy 1829 leTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlav 1849
Db 4954 TCCTCTTCGTGAGTACATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5013
Qy 1849 alLeuMetLysHisLeuGluSerAsnLysGluAlaLysGlu-----GluAlaG 1866
Db 5014 TCATCTTGGAGAACTTCAGCGTAGCCACAGAGAAAGCGCGATCTCTGAGCGAGCAG 5073
Qy 1866 luLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProL 1886
Db 5074 ACTTCGAGACTTCTTATGAG----- 5093
Qy 1886 euGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysP 1906
Db 5094 -----ATCTGGAGAGTTTGNAT----- 5111
Qy 1906 roGlyAlaProHisThrThrAlaHisIleGly-----AlaAlaSerGlyPheS 1922
Db 5112 -----CCTGATGCCACCCAGTTCATCGAGTACTGTAAAGTGGCGGATTTGCCGAGC 5163
Qy 1922 erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA 1942
Db 5164 CCTGGAGCATCCCGCTCGAGTACCCCAAGCCCAACACATCGAGCTC-----ATCCGCCATGG 5220
Qy 1942 spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT 1962
Db 5221 ACCTGCCCATGCTG-----AGCGGA---GATCGAATCCATGCTGTG-----GACATCC 5265
Qy 1962 yrMetCysArgAsnGlnSerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeuP 1982

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Db 5266 TTTTTC-----GCCTTCACCAAGCGAGTCTCTGGGACACAGTGGG----- 5303
Qy 1982 roLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI 2002
Db 5304 -----GAGTTGGACATCTCTCGGCGAGCAGATGGAGGACGGTTGCG 5343
Qy 2002 leLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpG 2022
Db 5344 TGGCGCTCAATCTCTCCAAAGTGTCTTAC----- 5372
Qy 2022 lyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgA 2042
Db 5373 -----GAGCTATACACACCACTCTCGCGCGCA 5400
Qy 2042 rgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspL 2062
Db 5401 AGCAG----- 5405
Qy 2062 euLeuSerGluValSerGlyPro-SerCysProLeuThrArgSerSerSerPheTrpGly 2081
Db 5406 -----GAAGAGGTGTCTGAGTGGTCTTACAGCGTCTTACAGGGGACACCTGGCTAGGC 5460
Qy 2082 GlySerSerIleGlnValGlnGlnArgSer-----GlyIleGlnSerLys 2096
Db 5461 GGGGCTTCA-----TCTGCAGAAAGATCACTTCCAAAGCTGGAGAATGGAGGCCACC 5514
Qy 2097 ValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLys 2116
Db 5515 ACCGAGAGAGAGAGAGACACCCCGTCCACAGCCTCCCTCCCTTTACGACAGCGTGA 5574
Qy 2117 AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly 2136
Db 5575 CAAAGCCCGACACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5604
Qy 2137 AspLeuLeuProSerSerGlnGlnGluProLeuPheProArgAspLeuLysLys 2154
Db 5605 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5646

RESULT 8
CF548698 879 bp mRNA linear EST 22-SEP-2003
LOCUS AGENCOURT_15594508 NICHDK_XGC_Brnl Xenopus laevis cDNA clone
DEFINITION IMAGE:7018586 5', mRNA sequence.
ACCESSION CF548698
VERSION CF548698.1 GI:349885530
KEYWORDS EST..
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 879)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue procurement:
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14738 row: j column: 24
High quality sequence stop: 646.
FEATURES
source 1..879
/organism="Xenopus laevis"
/mol_type="mRNA"

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/db_xref="taxon:8355"
/clone="IMAGE:701858"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC_Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN
Alignment Scores:
Pred. No.: 4.09e-78 Length: 879
Score: 1275.00 Matches: 250
Percent Similarity: 91.19% Conservative: 19
Best Local Similarity: 84.75% Mismatches: 17
Query Match: 10.60% Indels: 9
DB: 7 Gaps: 2

US-09-611-257A-24 (1-2287) x CF548698 (1-879)

Qy 1497 AspGlyTrpValAspLeuMetTyrAspGlyLeuAspAlaValGlyValAspGlnPro 1516
Db 1 GACGGATGGGTGGACATCATGTATGATGACTGCTGCTGGAATTCAGCAGACCA 60

Qy 1517 IleMetAsnHisAsnProTirpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAla 1536
Db 61 GTGATGATTAACACCCCTTGATGCTGCTATATTCATCTATTTTGTCTGATTTGGCA 120

Qy 1537 PhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGln 1556
Db 121 TTTTGTGCTCAACATGTTTGGTGTGTGGTGGAGAACTTCCATAAGTCGGCAG 180

Qy 1557 HisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgLeuGluLys 1576
Db 181 CATCAGGAGGAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240

Qy 1577 LysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAsp 1596
Db 241 AAGAGAGG-----AAGGCCCGAGTGTAAACCTACTATTCGGAG 279

Qy 1597 TyrSerArgPheArgLeuValHisLysCysThrSerHisTyrLeuAspLeuPhe 1616
Db 280 TATTCTCACCTTCGGCTCTCATCATCATGATCTGTACAGTCATTTATTTGATTTGTTT 339

Qy 1617 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1636
Db 340 ATTACTGGGGTCATTGGGATTTGAATTTATCTATGCAATGGAGCACTATCAGCAACCC 399

Qy 1637 GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe 1656
Db 400 CAGTATTGTTGAAGCTCTAAAATCTGTAAATACATCTTTTACCCTCATTTTCGTACTG 459

Qy 1657 GluSerValPheLysLeuValAlaPheAlaPheArgPhePheGlnAspArgTrpAsn 1676
Db 460 GAATCTGGTGCAGAAATGATAGCTTTTGGCTTCGGCGATTCCTTTAAAGCAGGTGGAAC 519

Qy 1677 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu 1696
Db 520 CAGTGTGATCTGGGCATCGTCTCTCCATCATGCGGAATCACACTGGAAGATTTGAA 579

Qy 1697 ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1716
Db 580 GTCAATGATCAGTCCCATTAACCAATCATCCGAATTAATGAGGCTTCCTCGGATTT 639

Qy 1717 AlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal 1736
Db 640 GCTCGGTGCTGAAGTTATTAAAGATGTCAGTGTGATGCGAGCCCTGCTGTGATCGGTT 699

Qy 1737 MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle 1756
Db 700 CTGAAGCGCTTCTCAAGTGGGAATCTCGGCCTGCTCTTTATGCTGCTGCTCTTTTAA 759

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Qy 1757 PheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys 1776
Db 760 TTTGCGCTCTGGGAGTTGAACCTTTTGGTGACTTAAAGACCACTGGATCCATCCCTGT 819

Qy 1777 Glu-GlyLeuGlyArgHisAlaThrPheArgAsn---PheGly 1789
Db 820 GAAAGGTCTTGGCAGACTTGCCACTTTTCAAGGAATTTTCGGG 862

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RESULT 9

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CA319705 793 bp mRNA linear EST 09-JUL-2003
LOCUS UI-M-FW0-cca-d-09-0-UI.r1 NIH BMAP_FW0 Mus musculus cDNA clone
DEFINITION IMAGE:6816826 5', mRNA sequence.
ACCESSION CA319705
VERSION CA319705.1 GI:24537829
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.

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FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6816826"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaudo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

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ORIGIN

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Alignment Scores:
Pred. No.: 6.7e-77 Length: 793
Score: 1256.50 Matches: 241
Percent Similarity: 92.40% Conservative: 2
Best Local Similarity: 91.63% Mismatches: 9
Query Match: 10.45% Indels: 11
DB: 6 Gaps: 1

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US-09-611-257A-24 (1-2287) x CA319705 (1-793)

Qy	1444	LeuPheLysGlyLysPheValCysGlnGlyGluAspThrArgAsnIleThrAsnLys	1461
Db	3	CTCTTCAAGGGAGATTCTTCGTGTGTTCAGGGTGAGACACCAAGGAACATCCTTAACAAG	62
Qy	1464	SerAspCysAlaGluAlaSerTyrArgTirpValArgHisLysTyrAsnPheAspAsnLeu	1483
Db	63	TCCGACTGTCTCTGAGGCCAGTTACCGGTGGTCCGGCACAAGTACAACTTTGACAACTG	122
Qy	1484	GlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTirpValAspIleMet	1503
Db	123	GGCCAGGCTCTGATGTCCCTGTGTGTCTGGCCCTCCAAGGATGGCTGGGTTCACATCATG	182
Qy	1504	TyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTirp	1523
Db	183	TATGATGGACTGGATGCTGTGGGAGTGGACAGCAGCCCATCATGAACCAACAAACCTTGG	242
Qy	1524	MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe	1543
Db	243	ATGCTGTCTACTTCATCTCCTCTCTCATCTGTGGCCCTCTTCGTCTGAAACATGTTT	302
Qy	1544	ValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluGluAla	1563
Db	303	GTGGCGCTGTGTGTGGAACTTCCATAAGTTCAGGAGCAGCACCAAGGAGGAGGAGGAGCG	362
Qy	1564	ArgArgGluGluLysArgLeuArgGluGluLysLysArgTg-----	1579
Db	363	CGGCGGGGAGGAGAAGCGACTAAAGAGGCTGGAGAAAGAGAGGAATCTAATGTTG	422
Qy	1580	-----SerLysGluLysGlnMetAlaGluAlaGlnCysLysPro	1592
Db	423	GACGATGTAATTGCTTCGGCAGCTCAGCCAGCGTCGTCAGAAAGCCAGTGCAAACCC	482
Qy	1593	TyrTyrSerAspTyrSerArgPheArgLeuValHisHisLeuCysThrSerHisTyr	1612
Db	483	TACTACTCTGACTACTCTCGGCTCCGCGTCCCTCGTCCACCACTGTGTACAGGACCATAC	542
Qy	1613	LeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHis	1632
Db	543	CTGGACCTCTTCATCCTCTGGTGTCTATCGGGCTGAAATGTGTCTCAATGGCCCATGGACAT	602
Qy	1633	TyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrVal	1652
Db	603	TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAACTACATCTTTACCGTC	662
Qy	1653	IlePheValPheGluSerValPheIysLeuValAlaPheAlaPheArgPhePheGln	1672
Db	663	ATCTTTGTCTTGGAGTCAGTATTTCANACTTGTGGCCCTTCGGCTCCCGCGGTCTTCACG	722
Qy	1673	AspArgTirpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeu	1693
Db	723	GACAGTGGAAACCACTGGACCTGGCTATGTGTCTTCTGTCCATCATGGGCATCAGCTG	782
Qy	1693	GluGluIle 1695	
Db	783	GAAGAGATT 791	

RESULT 10	AY116499	5943 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY116499				
DEFINITION	Homo sapiens SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY116499				
VERSION	AY116499.1	GI:39772459			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 5943)				
AUTHORS	Clark,A.G., Gланowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,				

TITLE	Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 5943)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.					
FEATURES	Location/Qualifiers source 1..5943 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" <1..>5943 /gene="SCN8A" /locus_tag="HCNM5911"					
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ORIGIN						
Alignment Scores:						
Pred. No.:	1.13e-73	Length:	5943			
Score:	1230.50	Matches:	520			
Percent Similarity:	36.92%	Conservative:	339			
Best Local Similarity:	21.84%	Mismatches:	840			
Query Match:	10.23%	Indels:	664			
DB:	9	Gaps:	83			
US-09-611-257A-24 (1-2287) x AY416499 (1-5943)						
Qy	25	ProProGlyProArgLeuAlaArgGlyThrTrpThrArgArgMetGluArgAlaProArg	44			
Db	22	CCACCAGGCCCTGATAGTTTCAAGCCTTTTCACC	-	CCTGAG	60	
Qy	45	SerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAla	64			
Db	61	TCACGTGCACAACATTGAGAGCGCCATGCTGAGAGCAAGCAAGCCAAACAGGGCC	12			
Qy	65	GlyAlaGlySerThrGluLysAspProGlySer	79	AlaAspSerGlu	79	
Db	121	GATGGCAGTCATCGGAGGACGATGAGGACAGCAAGCCCAAGCAACGACGACTGGAA	18			
Qy	80	Ala	83	GluGlyLeu	83	
Db	181	GCAGGGAAGAGTTTGCTTTCACTACGGGGACATCCCACAGGCCCTGTTGCAGTTCCC	24			
Qy	84	-----ProTyrr-----	88			
Db	241	CTGAGGACCTTTGACCCATACTATTGACGCAGAAAACCTTTGTAGTATTAAACAGAGGG	30			
Qy	86	-----ProAlaLeuAlaProValValPhePheTyLeu	99			
Db	301	AAAACTCTTTCAGATTTAGTGCACGCCCTGCCTTG	33	TACATTTTA	33	
Qy	97	SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGlu	117			
Db	346	AGTCCTTTTAACCTGATAAGAGAATAGCTATTAAAATTTTGATACATCATTTATTAGC	40			
Qy	117	ArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgPro	131			
Db	406	ATGATCATTATGTGCATATTATTTGACCAACTGTGTATTCATGACTTTTTAGTAAACCTCTCT	44			
Qy	136	-----CysGluAspIleAlaCysAspSerGlnArgCysArgileLeuGlnAlaPheAsp	151			
Db	466	GACTGGTGCAGAAATGTTG	47			
Qy	154	AspPheIlePhe---AlaPhePheAlaValGluMetValVallysMetValAlaLeuGly	171			

QY 792 rMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluLeuSerAs 812
Db 2307 NNN 2366
QY 812 nIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPr 832
Db 2367 NNNNGTTTTTCACTGGAAATTTTCACAGCGGAAATGTCCTGGAAGCTATAGCCATGATCC 2426
QY 832 oPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVa 852
Db 2427 CTACTATTATTTCAAGAAGTTGGAAACATTTTTCACGGATTATTTGCTCCCTCAGTTT 2486
QY 852 lTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMe 872
Db 2487 AATGGAAGCTAGCTAGCAGACGTGGAGGGCTTTTCAGTCTGCGATCTTTCCGATTGNN 2546
QY 872 tArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnValValLeuMe 892
Db 2547 NNN 2606
QY 892 tLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhelePh 912
Db 2607 NNNNNNNNNNNNNNNNNNGGCAACCTGACACTGGTCTGGCCATTATTGCTTCATCTT 2666
QY 912 eSerIleLeuGlyMetHisLeuPheGly-----CysLysPheAl 925
Db 2667 TGGCGTGGTGGGATGCACTTTTGGAAAAAGCTCAAGAGGTGTGCTGCAAGATCAA 2726
QY 925 aSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAl 945
Db 2727 CCAGGACTGGAA-----CTCCCT---CGCTGGCATATGCATGACTTTTCCATTC 2774
QY 945 aIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGl 965
Db 2775 CTTCCTCATTTGCTTTCGAGTGTGTGCGGGAG---TGGATTGAGACCATGTGGGACTG 2831
QY 965 yMet---AlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl 984
Db 2832 CATGGAAGTCGAGCGCCAGCCCATGTGCTCATTTGCTTTATGATGTCATGTGATTGG 2891
QY 984 yAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPhe----- 1000
Db 2892 CAACTTGGTGNNN 2951
QY 1000 ----- 1000
Db 2952 NNN 3011
QY 1000 ----- 1000
Db 3012 NNN 3071
QY 1001 -GlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPheSerProSerVa 1020
Db 3072 GCAGCGTGAGCTGATCAGTGGAAG----- 3096
QY 1020 lAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGl 1040
Db 3097 -----CCTCTGGATGAGTTGTATGA 3116
QY 1040 uLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHi 1060
Db 3117 AAAGAAGCCCAACTGTATC-----GCCAATCA 3143
QY 1060 s-ProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgThrS 1080
Db 3144 CACCGGTGCAGACATCCACCGGAATG----- 3169
QY 1080 eSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSerA 1100
Db 3170 -----GTGACTTTCCA 3179

QY 1100 lAArgSerSerProHisSerProTrpSerAlaAlaSerSerTrp-----ThrSerArgA 1118
Db 3180 GAAGATGCAATGGCACAACCGCGCATTTGGCAGCAGCGTGGAGAAATACATCATTT-G 3238
QY 1118 rGSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyG 1138
Db 3239 ATGAGGACCACATGCTCTTCATCAACAACCCCAACTTGACTGTACGGGTACCC----- 3291
QY 1138 luArgArgSerLeuLeuSerGlyGluGly-----GlnGluSerGlnAspGluGluS 1156
Db 3292 -----ATTGCTGTGGCGGAGTCTGACTTTTGAGAACCTCAACACAGAGGATGTTA 3340
QY 1156 eSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuG 1176
Db 3341 GCAGCGAGTCGGAT-----CCTGAAGGCGAGCAAAATAAATACTAGATGACACCAGCT 3391
QY 1176 luArgGluAlaLysSerSerPheAspLeu---ProAspThrLeuGlnValProGlyLeuH 1195
Db 3392 CCTCTGAAGGA---AGCACCATTTGATATCAACACCAAGTAGAAGAGGTCCCT----- 3441
QY 1195 iArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerA 1215
Db 3441 ----- 3441
QY 1215 lAsrGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspA 1235
Db 3442 -----GTGGAACACCTTGAGGAATACTTGGATCCAGATGCCT 3478
QY 1235 sPAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgL 1255
Db 3479 GCTTCACAGAAGGTGTGTCCAGCGGTTCAG----- 3510
QY 1255 euProAlaCysCysArgGluArg-----AspSerTrpSerAlaTyrI 1269
Db 3511 -----TGTCGCCAGGTCAACATCGAGGAAGGGCTAGCAAGTCTTG-----TGA 3556
QY 1269 lPheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetP 1289
Db 3557 TC-----CTCGGAAACCTGCTTCCTCATCGTGGAGCACAACTGGT 3598
QY 1289 hAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgP 1309
Db 3599 TTGAGACCTTCATCATCTTCATGATTCCTGTCAGCAGTGGCGCCCTTCGAGGACA 3658
QY 1309 rOlySileAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheT 1329
Db 3659 TCTACATTGAGCAGAGAAAGACCATCCGCCATCTCGGAATATGCTGCAAAAGTCTTCA 3718
QY 1329 hrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyG 1349
Db 3719 CCTATATCTTCCTCGGAGATGTTGCTCAAGTGGACAGCTATGCTTGC----- 3771
QY 1349 luGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLeuSerV 1369
Db 3772 -----AAGTCTTCACCAATGCTGCTGTGGTGGACTTCCTCATTTGTGGTNNNNNN 3826
QY 1369 aIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuA 1389
Db 3827 NNN 3886
QY 1389 rgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyL 1409
Db 3887 NNN 3937
QY 1409 euLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValI 1429
Db 3938 NNNNNGTGTGTGTAATGCTTGTGGTGGCGCCATCCCTCCCATCATCAATGTGCTGCG 3997
QY 1429 leCysCysAlaPheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysP 1449
Db 3998 TGTGCTCTATCTCTCGCTGATTTTCAGCATCATGGGATTAACCTGTTTTCGCGGAAGT 4057
QY 1449 hPheValCysGlnGlyGlu-----AspThrArgAsnIleThrAsnL 1463

[illegible]

5093	Db	TGTTTCAAAATCAACACTCAGCTGGTGTGGATGGCGCTGCTGTGCGCCATCTCTAAACCGCC	5155
1810	Qy	spProSerArgAspCysAspGlnGlu-----SerThrCysTyra	1823
5153	Db	CCCTGACTGCACCTAGATAAGGAACCCAGGAGTGGCTTTAAGGAGATTGTGGGA	5212
1823	Qy	snThrValIleSerProIleTyrrPheValSerPheValLeuThrAlaGlnPheValLeuV	1843
5213	Db	ACCCCTCAGTGGGCATCTCTCTTTGTAAAGCTACATCATCATCTCTCTCTAAATGTCTG	5272
1843	Qy	alaenValValIleAlaValLeuMetLysHisLeuGluGluSerAenLysGluAlaLysG	1863
5273	Db	TGAACATGTACATTCGTCATCTCTGGAGAACCTCAGTAGTGCACAGAGAAAGTGCAG	5332
1863	Qy	lu-----GluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerP	1880
5333	Db	ACCCTCTGAGTGAGGATGACTTTGAGACCTTCTATGAG-----	5370
1880	Qy	roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS	1900
5371	Db	-----ATCTGGGAGAAAGTTCGAC-----	5388
1900	Qy	erThrAspSerProLysProGlyAlaProHisThrAlaHisIleGly-----	1916
5389	Db	-----CCGATGCCACCAGTTCAITGAGTACTGTAAAGC	5422
1917	Qy	--AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValP	1936
5423	Db	TGCGACACTTGGAGATGCTTGGAGCATCTCTCCGAGTGCCCAAGCCAAATACCATTG	5482
1936	Qy	roValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHis	1956
5483	Db	AGCTC--ATCGCTATGATCTGCCAATGGTG-----AGCGGG--GATCGCATCCACT	5530
1956	Qy	erLeuProAsnAspSerTyrrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyH	1976
5531	Db	GCCTG-----GACATCTCTTTT-----GCCTTCACCAAGCGGCTCTCGGAG	5572
1976	Qy	isArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnP	1996
5573	Db	ATAGCGGG-----GAGTTGGACATCTCTCGCGCAGC	5602
1996	Qy	roAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrrLeuLeuGlnProH	2016
5603	Db	AGATGAAGAGCGGTCGTGGCATCCCAATCTCTCCAAAGTGTCTTAC-----	5649
2016	Qy	isGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuA	2036
5650	Db	-----GAGCCCAATCA	5659
2036	Qy	laGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyL	2056
5660	Db	CAACCACTGCGTCCGACGAG-----	5682
2056	Qy	euGlySerArgGluAspLeuLeuSerGluValSerGlyPro-SerCysProLeuThrArg	2075
5683	Db	-----GAGGAGGTATCTGCAGTGGTCTCTGCAGCGTGCCT---	5716
2076	Qy	serSerSerPheTrpGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSer	2095
5717	Db	ACCGGGGACATTTGGCAAGCGGGGCTTCATCTGCAAAAGAACCACTCTTAATAGCTGG	5776
2096	Qy	lysValSerIlyHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAla	2115
5777	Db	AGAATGAGGCACACACCGGGAGAAAAAGAGACGCCCTCATCTACAG-----	5824
2116	Qy	lysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSer	2135
5825	Db	-----CCTCCCTCCCTCTATGACAGTGTAACTAACTGAAAGAGGAAACACGACGC	5878
2136	Qy	GlyAspLeuLeuProSerSerGlnGluProLeuPheProArgAspLeuLysIys	2154
5879	Db	GGG-----CAGAGGAAAGGAAAGGAAAGAGCCAAAGACAAAAAGAGG	5923

QY	958	TrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPhe	977
Db	123	TGGAATAAAGCTTTTACACCGGATGGCTCCACGTCATCTTTGGGCTGCTTTTACTTC	182
QY	978	IleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuVal	997
Db	103	ATCGCCCTCATGACTTTTGGCAACTAGTGCTCTTTAACTGCTTTGTGCGCATCTTCGTG	242
QY	998	GluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPheSer	1017
Db	243	GAGGCTTTCCAGGCGAGGAGATGCCACCAAGTCTGAGTCAGAGCGTGAATTTCTTCG	302
QY	1018	ProSerValAspGlyAspGlyAspArgLysArgLeuAlaLeuValAlaLeuGlyGlu	1037
Db	303	CCCAGTGTGGATGTGTATGGGGCAGGAAGCGCTTGGCCCTGTGGCTTTGGGAGAA	362
QY	1038	HisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrPro	1057
Db	363	CACTCGGAACATACGAAGAGGCTTTTGGCACTCTCATATCCACAGCTGTACACG	422
QY	1058	MetSerHisProLysSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArg	1077
Db	423	ATGTCACCTGCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTTGGGCTCTGCG	482
QY	1078	ArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysPro	1097
Db	483	CGCACCATGACGTGGGTCCGCTGAGCTGGAACTCCCATCATGATGATGAATCACCG	542
QY	1098	ProSerAlaArgSerSerProHisSerProTrioSerAlaAlaSerSerTrpThrSerArg	1117
Db	543	CCAAAGTGCCTCCAGAGCTCCCGCACAGTCCCTGGAGCGCAGCAGCAGTGGACGAGG	602
QY	1118	ArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgSerProSerGly	1137
Db	603	CGCTCCAGCCGGAACAGCTGGGCGGGCGGCCCCCAAGCGCTGAAGCGTGAAGCCGAGG	662
QY	1138	GluArgArgSerLeuLeuSerGlyGlyGlyGlnSerGlnAspGluGlu	1154
Db	663	GAGCGAGGTCCTCTGTCTGGAGAGGGTCAGAGAGCCAGGATGAGGAG	713
RESULT 12			
LOCUS	BU709095	810 bp mRNA linear	EST 15-JUL-2003
DEFINITION	UI-M-EW0-caz-e-20-0-UI.r1.NIH_BMAP_EW0 Mus musculus CDNA clone		
ACCESSION	IMAGE:6419323 5', mRNA sequence.		
VERSION	BU709095		
KEYWORDS	EST.		
SOURCE	BU709095.1 GI:23642225		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	1 (bases 1 to 810)		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: Dr. James Lin, University of Iowa		
	CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa		
	CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LINL at:		
	http://image.llnl.gov		
	This clone was contributed by the Brain Molecular Anatomy Project		
	(BMAP)		
	Seq primer: PYX-5.		
FEATURES	Location/Qualifiers		
source	1..810		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
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	/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;		
	Site 2: Not I; The library was constructed according		
	Bonaldi, Lennon and Soares, Genome Research, 6:791-806,		
	1996. Denatured RNA was size fractionated on a 1% agarose		
	gel. First strand cDNA synthesis was primed with oligo-dT		
	primer containing a Not I site. Double strand cDNA was		
	size selected according to mRNA size fraction, ligated with		
	EcoR I adaptor, digested with NotI and then cloned		
	directionally into pYX-Asc vector. The library tag		
	sequence located between the Not I site and the polyA tail		
	is CGACTGAT. This library was created for the University		
	Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the		
	Developing Mouse Nervous System', supported by National		
	Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,		
	program coordinator."		
ORIGIN			
Alignment Scores:			
Pred. No.:	6.63e-73	Length:	715
Score:	1198.00	Matches:	233
Percent Similarity:	98.73%	Conservative:	1
Best Local Similarity:	98.31%	Mismatches:	3
Query Match:	9.96%	Indels:	0
DB:	7	Gaps:	0
US-09-611-257A-24 (1-2287) x CF745071 (1-715)			
QY	918	HisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLys	937
Db	3	CACCTTTTGTGTGCACTGATGCGGATGGGACACGTTCCAGACCGGAG	62
QY	938	AsnPheAspSerLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAsp	957
Db	63	AAATTTTGAATCCCTGCTGGGCCATGTGACTGTCTTTCAGATTCTGACTCAGGAAGAC	122


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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6419323"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH_BMAP_EWO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GGGCTGGNA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 9.53e-73 Length: 810
Score: 1197.00 Matches: 246
Percent Similarity: 91.51% Conservative: 2
Best Local Similarity: 90.77% Mismatches: 11
Query Match: 9.95% Indels: 15
DB: 5 Gaps: 1

US-09-611-257A-24 (1-2287) x BU709095 (1-810)

Qy 1369 ValLeuAspLeuValSerMetValSerAspSerGlyThrLysLeuGlyMetLe 1388
Db 1 GTCATCGACATCCCTGTGTCTCATGCTCTGACAGCGGCACCAAGATTCGCGCATGCT 60

Qy 1388 uArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValLeuSerArgAlaGlnGl 1408
Db 61 GAGGGTGTGGGCTGCTGGGACCCCTACGTCCATCAGGGTCAATCAGCGGGCCAGGG 120

Qy 1408 YLeuLysLeuValValGluThrLeuMetSerSerLeuLysProLeuGlyAsnLeuValVa 1428
Db 121 GCTGAAGCTGTGGTAGAGACTCTGATGTCATCCCTCAAAACCCATTTGCAACATTTGGT 180

Qy 1428 lIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLy 1448
Db 181 CATCTGCTGCTCTCTTCATCATTTTTGGAAATCTTGGGGTGCAGCTCTTTCAAAGGGAA 240

Qy 1448 sPhePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGl 1468
Db 241 GTTCTTCTGTGTGAGGGTGAAGACACAGAGAAATCATCTAACAGTCCGACTGTGCTGA 300

Qy 1468 uAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMe 1488
Db 301 GGCCAGTTACCGTGGGTCCGGCAACAGTCAACACTTTGACAACTGGGCCAGGCTCTGAT 360

Qy 1488 tSerLeuPheValLeuAlaSerLysAspGlyTyrPheValAspIleMetTyrAspGlyLeuAs 1508
Db 361 GTCCCTGTGTTGTGGCTCCCAAGGATGGCTGGGTTGACATCATGTATGATGACTGGA 420

Qy 1508 pAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPh 1528
Db 421 TGCTGTGGGATGGACACGAGCCCATCATGAACCAACCCCTTGGATGCTGCTCTACTT 480

Qy 1528 eIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValVa 1548
Db 481 CATCTCTCTCTCTCATCGTGGCTTCTTCTGCTCTGAACATGTTTGGGCGTGGTGGT 540

Qy 1548 lGluAsnPheHisLysCysArgGlnHisGlnGlnGluGluAlaArgArgGluGl 1568
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6419323"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (TI phage resistant)"
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/notes="Organ: brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GGGCTGGNA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 1.57e-72 Length: 952
Score: 1195.50 Matches: 250
Percent Similarity: 81.88% Conservative: 3
Best Local Similarity: 80.91% Mismatches: 31
Query Match: 9.94% Indels: 25
DB: 7 Gaps: 7

US-09-611-257A-24 (1-2287) x BU709095 (1-810)

Qy 1568 uLysArgLeuArgArgLeuGluLysLysArgArg 1579
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Qy 1580 -----SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTy 1597
Db 661 TTCCGGCAGCTCAGCCAGCGCTCGCTCAGAACCCAGTGCANACCTACTACTCTGACTA 720

Qy 1597 rSerArgPheArgLeuLeuValHisLeuCysThrSerHisTyrLeuAspLeuPheIl 1617
Db 721 CTCGGCTTCGGCTCCC-TCGTCACACCTGTGTACAGC-CACTACCTGNA-CTCTTCAT 777

Qy 1617 eThrGlyValIleGlyLeuAsnValValThr 1627
Db 778 CACTGGTGTATCGGGCTGAATGTGGTCAG 808

CF584866 952 bp mRNA linear EST 24-SEP-2003
AGENCY: 11360281 updated NIH_MGC_137 Mus musculus cDNA clone
IMAGE: 6431076 5', mRNA sequence.
CF584866
VERSION CF584866.1 GI:35198128
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 952)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-x@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 p1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: INBD12 row: f column: 01
High quality sequence start: 15
High quality sequence stop: 571.
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/lab_host="DH10B"
/clone_lib="NIH_MGC_137"
/notes="Organ: pancreas; Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Library consists of a pool of clones rearranged from the following libraries: Melton normalized mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse islets 1 MMS1-A, and Kaestner ngn3 wt. Clones rearranged in the laboratory of K. Kaestner (University of Pennsylvania). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 1.57e-72 Length: 952
Score: 1195.50 Matches: 250
Percent Similarity: 81.88% Conservative: 3
Best Local Similarity: 80.91% Mismatches: 31
Query Match: 9.94% Indels: 25
DB: 7 Gaps: 7

```

US-09-611-257A-24 (1-2287) x CF584866 (1-952)

Qy	1746	LeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPhe	1765
Db	34	CTGGGACTCTCTTCAATGATATATATTTTCACTTTGACGCTTGGGGTGGAGCTCTTT	93
Qy	1766	GlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPhe	1785
Db	94	GGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGGCGCGCATGCCACCTTT	153
Qy	1786	ArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsn	1805
Db	154	AGAACTTGGTATGGCTTTTCGACCCCTTCCGAGTCTCCACTGGTGACACCTGGAAAT	213
Qy	1806	GlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrVal	1825
Db	214	GGTATATGAGGACACCTCCGGGACTGTGACAGGAGTCCACCTGTACAAACCCGTC	273
Qy	1826	IleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVal	1845
Db	274	ATCTCACCCATCTACTCTGCTGCTCTGCTGACGGCCAGTTTGTGCTGCTCAACGTG	333
Qy	1846	ValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluAla	1865
Db	334	GTATAGCCGTGCTGTATGAGACACCTTGGAGAGGACAAAGAGAGCCAGGAGGCG	393
Qy	1866	GluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnProHisSerPro	1885
Db	394	GAGTGGAGCGGAGCTGGAGCTAGAGATGAAGACACTCAGCCGCGAGCCCACTCCCG	453
Qy	1886	LeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLys	1905
Db	454	CTGGGACGCCCTTCTCTGCTGGGTGGAGGTGCAATAGCCCTTGACAGCCCTAAG	513
Qy	1906	ProGlyAlaProHisThrAlaHisIleGlyAlaAla---SerGlyPheSerLeuGlu	1924
Db	514	CTGGGGCTCACACACACAGGCCCATTTGGAGAGCCTCTTCAGGCTTCTCCCTTGA	573
Qy	1925	HisProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeu	1944
Db	574	CACCCACGATGTATCTCACACTGAGAGGGGGCCAGTCCCTTAAGACAGACCTGCTG	633
Qy	1945	ThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCys	1964
Db	634	ACTGTGAGGAAGTCTGGTGTGAGCGGACACACTCTCTGCCCAATGACACTACATGTC	693
Qy	1965	ArgAsn-GlySerThrAla-GluArgSerLeuGlyHisArgGlyTrpGlyLeu---ProL	1983
Db	694	CGCAATGGGAGCCCTGCCGAGAGATCCCTTAAGACACAAAGGGGCTGGGGCCCTCC	753
Qy	1983	ysAlaGlnSerGly---SerIleLeuSerValHisSerGlnProAlaAspThrSerCysI	2002
Db	754	AAGCCCACTAGGGCTCCAATCTTGTCTGTCTACTCTCCCAACCAACGAGAACAC	809
Qy	2002	leLeuGlnLeu-----ProLysAspValHisTyrLeuLeuGlnProH	2016
Db	810	-----CAGCTGGCATCTAAAGCTTTCCTCCCAAAATGCCCCA-----CTATCTGGGT	858
Qy	2016	isGlyAlaProThrTrpGlyAlaLePro-----LysL	2027
Db	859	TCCGAGCCCTCTCTTGGGGGGCGTCCCAACCTGGGGGGGGCGCTACCTCCCTCTTAA	918
Qy	2027	euProProGlyArgSerPro	2034
Db	919	TAACCCCTCCCACTTGGGGCCC	941

RESULT 14

AK083220

LOCUS

DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone: C630029C19 product: sodium channel, voltage-gated, type VIII, alpha polypeptide, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

TITLE
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MEDLINE
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REFERENCE
AUTHORS

TITLE
JOURNAL
REFERENCE
AUTHORS

COMMENT

AK083220
AK083220.1 GI:26101130
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Iashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hara, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4675)
Adachi, J., Aizawa, K., Akimura, T., Atakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/

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found through the I.M.A.G.E. Consortium/ILNL at:
http://image.lnli.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
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Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

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Best Local Similarity: 93.70% Mismatches: 15
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US-09-611-257A-24 (1-2287) x BU058818 (1-771)

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